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20 NOV 2006

Docket No. 12810-00067-US
(PATENT)

Legal Staff
International Division

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:
Karl-Heinz Kogel et al.

Application No.: 10/522,106

Confirmation No.: 9243

Filed: January 24, 2005

Art Unit: N/A

For: METHOD FOR OBTAINING THE
PATHOGENIC RESISTANCE IN PLANTS

Examiner: Not Yet Assigned

REQUEST FOR RECONSIDERATION

MS PCT Legal Affairs
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

The Applicants respectfully request reconsideration of the Decision on Petition mailed October 2, 2006. Applicants respectfully request reconsideration of the Request for Withdrawal of Holding of Abandonment, or in the alternative that the Petition under 37 CFR § 1.137 (b) be granted, and the application be forwarded to the Examiner for Examination.

**I. Request For Reconsideration of the Request for Withdrawal of Holding of
Abandonment**

In the Decision On Petition mailed October 2, 2006, the PCT Legal Examiner asserted that because the "Assignment of Application" allegedly did not specifically identify the application being assigned, that the submission of Power of Attorney and change of correspondence address submission of June 3, 2005, "did not properly establish the right of the assignee to take action in this case, and so the submission was not effective in changing the pre-existing correspondence address of record." Applicants respectfully disagree and strongly urge reconsideration of the Request for the following reasons.

1. The “Assignment of Application” was submitted with the initial filing of the application on January 24, 2005, as evidenced by the date on the Recordation Form Cover Sheet (attached as Exhibit 1 with the “Assignment of Application”; previously submitted in the Request for Withdrawal of Holding of Abandonment filed on April 28, 2006 as part of Exhibit A). The date on the cover sheet is January 24, 2005, which is the same as the date of filing of the application. The U.S. application number could only be given out after the initial filing of the application. Therefore, on the initial filing date of the application which included the “Assignment of Application” with the proper cover sheet, it would have been impossible for the U.S. application number to be indicated.

2. The inventors signed the “Assignment of Application” on July 30, 2003, shortly after the international filing date of July 14, 2003, assigning their entire rights to BASF Plant Science GmbH. Therefore, at the time of filing the U.S. national stage application on January 24, 2005, the “Assignment of Application” was already executed and could not have specifically identified the application by its U.S. application number.

3. Furthermore, toward the top right hand corner of each page of the “Assignment of Application” document, the number “0000053765” is printed (see Exhibit 1). This number represents the assignee’s internal docket number. This same number also appears as a header on the specification as filed. This same number also appears on the top right hand corner of each page of the “Declaration, Power of Attorney and Petition” (attached as Exhibit 2). This Declaration was signed by the inventors on the same day as the “Assignment of Application” on July 30, 2003 and was also submitted to the U. S. Patent and Trademark Office with the initial filing of the application on January 24, 2005. Therefore, the “Assignment of Application” does specifically identify the application which is being assigned, contrary to the Examiner’s assertion.

4. Since the Power of Attorney and change of correspondence address submission of June 3, 2005, Applicants received the Notice of Recordation of Assignment Document on November 8, 2005, indicating that the “Assignment of Application” was recorded in the U.S. Patent and Trademark Office on January 24, 2005 (attached as Exhibit 3). Such recordation can be found at Reel/Frame No. 016749/0176. The date of recordation corresponds to the date on the

recordation cover sheet and the date of the initial U.S. filing. The assignee of record is BASF Plant Science GmbH as of January 24, 2005, the date of filing the initial application. Therefore, when the Power of Attorney and change of correspondence address was submitted to the U.S. Patent and Trademark Office, BASF Plant Science GmbH was already the assignee of record with the authority and power to revoke previous powers of attorney and appoint new attorneys pursuant to 37 CFR § 3.71. Furthermore, when the Power of Attorney and change of correspondence address was submitted to the U.S. Patent and Trademark Office, the Transmittal of Power of Attorney indicated that the cover sheet and "Assignment of Application" document were enclosed because the Notice of Recordation had not yet been received and that these had been submitted with the initial filing of the application (as also indicated on the initial Request for Withdrawal of Holding of Abandonment). Therefore, the submission of the Power of Attorney and change of correspondence address was not to establish the rights of the assignee, since these were already established with the initial filing of the application, but to appoint new attorneys and change the correspondence address. Additionally, as required, a Statement under 37 CFR § 3.73(b) and a duly completed and executed "Power of Attorney to Prosecute Applications Before the USPTO" form were submitted pursuant to 37 CFR § 3.71 with the Transmittal of Power of Attorney.

5. Because the "Assignment of Application" was submitted with the initial filing of the application and identified the application by number, which number is found on the executed Declaration (Exhibit 2) and in the application as filed and because the "Assignment of Application" was duly recorded as of the application initial filing date of January 24, 2005 (as evidenced on the Notice of Recordation, Exhibit 3), Applicants submit that the Power of Attorney and change of correspondence address of June 3, 2005 appointing Connolly Bove Lodge & Hutz LLP was properly submitted by the assignee of record, BASF Plant Science GmbH.

6. A Notice of Missing Parts was mailed July 1, 2005 to Morrison & Foerster. BASF Plant Science GmbH appointed Connolly Bove Lodge & Hutz LLP with the Power of Attorney and change of correspondence address submission of June 3, 2005. Therefore, the Notice of Missing Parts was mailed to the incorrect address of record, which ultimately caused the application to go abandoned.

Applicants respectfully submit that the "Assignment of Application" submitted with the initial filing of the application on January 24, 2005 was effective in establishing the right of the assignee to take action in this case, for the reasons explained above.

Applicants respectfully request reconsideration of the Request for Withdrawal of Holding of Abandonment, because Applicants submitted a proper Power of Attorney with change of correspondence address, as explained above, prior to the mailing of the Notice of Missing Parts. Accordingly, Applicants also request reimbursement of the petition fee under § 1.17(m).

II. In the Alternative, Reconsideration of the Petition under 37 C.F.R. § 1.137 (b)

Further to the Decision On Petition mailed October 2, 2006, Applicants submit herewith a proper reply to the Notification to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures which the Examiner kindly provided with their Decision On Petition. The Reply consists of a copy of the Notification to Comply, a Response to the Notification to Comply and Amendment, a replacement paper copy of the Sequence Listing which conforms to 37 CFR §§ 1.821-1.825, a diskette containing the Sequence Listing in computer readable form, and a Statement to Support Filing and Submission in Accordance with 37 CFR §§ 1.821-1.825.

Although Applicants strongly urge reconsideration of the Request for Withdrawal of Holding of Abandonment, in the alternative, Applicants request that the Application be revived. The Petition fee has been paid. Applicants state that the entire delay in filing the required reply from the due date for the reply until the filing of a grantable petition pursuant 37 CFR § 1.137(b)(3) was unintentional. Applicants submit that with the attached reply all requirements under 37 CFR § 1.137(b) have been met.

Furthermore, Applicants respectfully request that a Notice of Acceptance of Power of Attorney be issued and the correspondence address be appropriately changed. If the Examiner finds that the Power of Attorney and change of correspondence address is not effective in

making these changes, then Applicants respectfully request assistance in what further would be required.

This response is filed within the two-month period for response from the mailing of the Decision on Petition, to and including December 4, 2006, pursuant to 37 CFR § 1.7(a). No fee is believed due. However, if a fee is due, the Commissioner is hereby authorized to charge or credit our Deposit Account No. 03-2775, under Order No. 12810-00067-US from which the undersigned is authorized to draw.

A prompt and favorable action is earnestly solicited.

Respectfully submitted,

By Roberte Makowski

Roberte M. D. Makowski

Registration No.: 55,421

CONNOLLY BOVE LODGE & HUTZ LLP

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1007 North Orange Street, P.O. Box 2207

Wilmington, Delaware 19899

(302) 888-6410 (Tel), (302) 658-5614 (Fax)

Attorney for Applicants

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20 NOV 2006

PTO/SB/92 (09-04)

Approved for use through 07/31/2006. OMB 0651-0031
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

Legal Staff
International Division
Application No.: 10/522,106

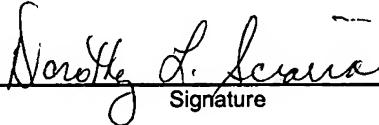
Attorney Docket No.: 12810-00067-US

Certificate of Mailing under 37 CFR 1.8

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to:

MS PCT
ATTENTION : PCT Legal Office
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

on November 15, 2006
Date


Signature

Dorothy L. Sciarra
Typed or printed name of person signing Certificate

Registration Number, if applicable

(302) 658-9141
Telephone Number

Note: Each paper must have its own certificate of mailing, or this certificate must identify each submitted paper.

Request for Reconsideration (5 pages)

Exhibit 1 – Recordation Form Cover Sheet and Assignment of Application (3 pages)

Exhibit 2 – Declaration, Power of Attorney and Petition (3 pages)

Exhibit 3 – Notice of Recordation and Assignment Document (3 pages)

Response to Notification to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures and Amendment (3 pages)

Copy of Notification to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures (9 pages)

Sequence Listing (CRF copy – 1 Disk and Paper copy (54 pages))

Statement to Support Filing and Submission in Accordance with 37 CFR §§1.821 through 1.825 (2 pages)

Certificate of Mailing (1 page)

Postcard



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
 United States Patent and Trademark Office
 Address: COMMISSIONER FOR PATENTS
 P.O. Box 1450
 Alexandria, Virginia 22313-1450
www.uspto.gov

U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/522,106	Karl-Heinz Kogel	532622010500

INTERNATIONAL APPLICATION NO.	
PCT/EP03/07589	
IA. FILING DATE	PRIORITY DATE

Morrison & Foerster
 1650 Tysons Boulevard, Suite 300
 McLean, VA 22102

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20 NOV 2006

Legal Staff
 International Division

CONFIRMATION NO. 9243

371 FORMALITIES LETTER



OC000000016430884

Date Mailed: 07/01/2005

**NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
 CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- For Rules Interpretation, call (571) 272-0951
- For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.
- Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

A copy of this notice MUST be returned with the response.

LAMONT M HUNTER

Telephone: (703) 308-9140 EXT 201

PART 2 - OFFICE COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/522,106	PCT/EP03/07589	532622010500

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/522,106
Source: PCT
Date Processed by STIC: 2-2-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005

TIME: 15:31:41

Input Set : A:\Sequence Listing.txt
 Output Set: N:\CRF4\02022005\J522106.raw

2 <110> APPLICANT: Kogel, Karl-Heinz
 3 Huckelhoven, Ralph
 4 Trujillo, Marco
 6 <120> TITLE OF INVENTION: Method for Obtaining a Pathogen Resistance in Plants
 8 <130> FILE REFERENCE: 532622010500
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/522,106
 11 <141> CURRENT FILING DATE: 2005-01-24
 13 <160> NUMBER OF SEQ ID NOS: 24
 14 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

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 47 <212> TYPE: PRT
 48 <213> ORGANISM: Hordeum vulgare
 W--> 49 <400> SEQUENCE: 2
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 51 1 5 10 15
 52 Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
 53 20 25 30
 54 Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
 55 35 40 45
 E--> 56 Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
 57 50 55 60
 58 Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
 59 65 70 75 80
 60 Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
 61 85 90 95
 62 Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
 63 100 105 110
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 2183 <212> TYPE: PRT
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 W--> 2185 <400> SEQUENCE: 16
 2186 Met Gln Asn Ser Glu Asn His His Pro His His Gln His His Ser
 2187 1 5 10 15
 2188 Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser Gly Pro Leu
 2189 20 25 30
 2190 Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn
 2191 35 40 45

P/S exp /AIN
 " location. Does Not Comply
 Corrected Diskette Needed
 (PG.1, 3)
 See error explanation
 on PAGE 5.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005

TIME: 15:31:42

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 2195 65 70 75 80
 2196 Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu
 2197 85 90 95
 2198 Asp Pro Glu Leu Ala Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr
 2199 100 105 110
 2200 Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val
 2201 115 120 125
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 2207 165 170 175
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 2209 180 185 190
 2210 Pro Arg Ala Lys Phe Gly Glu Cys Ile Gly Met Asn Lys Glu Ser Lys
 2211 195 200 205
 2212 Glu Phe Ala Val Glu Leu Tyr Asp Ala Leu Ala Arg Arg Arg Asn Ile
 2213 210 215 220
 2214 Thr Thr Asp Ser Ile Asn Lys Ala Gln Leu Lys Glu Phe Trp Asp Gln
 2215 225 230 235 240
 2216 Val Ala Asp Gln Ser Phe Asp Ser Arg Leu Gln Thr Phe Phe Asp Met
 2217 245 250 255
 2218 Val Asp Lys Asp Ala Asp Gly Arg Ile Thr Glu Glu Glu Val Arg Glu
 2219 260 265 270
 2220 Ile Ile Gly Leu Ser Ala Ser Ala Asn Arg Leu Ser Thr Ile Gln Lys
 2221 275 280 285
 2222 Gln Ala Asp Glu Tyr Ala Ala Met Ile Met Glu Glu Leu Asp Pro Asn
 2223 290 295 300
 2224 Asn Leu Gly Tyr Ile Met Ile Glu Asn Leu Glu Met Leu Leu Leu Gln
 2225 305 310 315 320
 2226 Ala Pro Asn Gln Ser Val Gln Arg Gly Gly Glu Ser Arg Asn Leu Ser
 2227 325 330 335
 2228 Gln Met Leu Ser Gln Lys Leu Lys His Thr Gln Glu Arg Asn Pro Ile
 2229 340 345 350
 2230 Val Arg Trp Tyr Lys Ser Phe Met Tyr Phe Leu Leu Asp Asn Trp Gln
 2231 355 360 365
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 2233 370 375 380
 2234 Thr Trp Lys Tyr Ile Gln Tyr Lys Glu Lys Ala Ala Tyr Lys Val Met
 2235 385 390 395 400
 2236 Gly Pro Cys Val Cys Phe Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu
 2237 405 410 415
 2238 Asn Met Ala Ile Ile Leu Phe Pro Val Cys Arg Asn Thr Ile Thr Trp
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005

TIME: 15:31:42

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Output Set: N:\CRF4\02022005\J522106.raw

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2243	450	455	460
2244	Ile His Gly Leu Ser His Leu Thr Cys Asp Phe Pro Arg Leu Leu Asn		
2245	465	470	475
2246	480	485	490
2247	495	500	505
2248	510	515	520
2249	525	530	535
2250	540	545	550
2251	555	560	565
2252	570	575	580
2253	585	590	595
E--> 2254	Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His Leu Phe Val Ile Val		
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2256	605	610	615
2257	620	625	630
2258	635	640	645
2259	645	650	655
2260	655	660	665
2261	670	675	680
2262	685	690	695
2263	700	705	710
2264	720	725	730
2265	735	740	745
2266	750	755	760
2267	765	770	775
2268	780	785	790
2269	795	805	810
2270	800	810	815
2271	815	820	825
2272	830		

↙
 P/S
 explain
 Xga location.
 P/S see
 error explanation
 on page 5.

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING DATE: 02/02/2005
PATENT APPLICATION: US/10/522,106 TIME: 15:31:42

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\02022005\J522106.raw

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2291 835 840 845
2292 Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln Ser Leu His
2293 850 855 860
2294 His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Lys Ser
2295 865 870 875 880
2296 His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg Ile Ala Leu
2297 885 890 895
2298 Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly Ala Pro Ala
2299 900 905 910
2300 Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser His Lys Thr
2301 915 920 925
2302 Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe
2303 930 935

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005
TIME: 15:31:43

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Output Set: N:\CRF4\02022005\J522106.raw,

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

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Seq#:2; Xaa Pos. 55
Seq#:15; N Pos. 1952
Seq#:15; Xaa Pos. 547
Seq#:16; Xaa Pos. 547

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005

TIME: 15:31:43

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Output Set: N:\CRF4\02022005\J522106.raw

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L:15 M:283 W: Missing Blank Line separator, <210> field identifier
L:19 M:283 W: Missing Blank Line separator, <220> field identifier
L:23 M:283 W: Missing Blank Line separator, <400> field identifier
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:193
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
L:56 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
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L:255 M:283 W: Missing Blank Line separator, <400> field identifier
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RECEIVED

SEQUENCE LISTING

<110> Kogel, Karl-Heinz
Huckelhoven, Ralph
Trujillo, Marco

20 NOV 2006
Legal Staff
International Division

<120> Method for Obtaining the pathogenic resistance in plants

<130> 12810-00067-US

<140> US 10/522,106

<141> 2005-01-24

<160> 24

<170> PatentIn version 3.3

<210> 1

<211> 337

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<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

<400> 1

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att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct 97
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
20 25 30
cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
35 40 45
ggt gtc gat gta gtg tct ggm act cga gtc cgg aca cat ttt gca aga 193
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
50 55 60
cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
65 70 75 80
gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa 289
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
85 90 95
cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
100 105 110

<210> 2

<211> 112

<212> PRT

<213> Hordeum vulgare

<220>

<221> misc_feature

<222> (55)..(55)

<223> The 'Xaa' at location 55 stands for Gly.

<400> 2

Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile

1	5	10	15												
Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala
		20				25					30				
Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu	Gln	Ala	Leu	Asn	His	Ala	Lys	Asn
		35				40					45				
Gly	Val	Asp	Val	Val	Ser	Xaa	Thr	Arg	Val	Arg	Thr	His	Phe	Ala	Arg
		50				55				60					
Pro	Asn	Phe	Lys	Arg	Val	Leu	Ser	Lys	Val	Ala	Ala	Lys	His	Pro	Tyr
		65				70				75			80		
Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu
		85							90					95	
Leu	Ser	Asn	Leu	Cys	His	Glu	Phe	Asn	Gly	Lys	Cys	Thr	Thr	Lys	Phe
		100						105					110		

<210> 3
<211> 2832
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (1)..(2829)
<223> coding for NADPH oxidase

<400> 3	48															
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Met	Arg	Gly	Gly	Ala	Ser	Ser	Gly	Pro	Gln	Arg	Trp	Gly	Ser	Ala	Gly	
1	5													15		
acg	aca	ccg	cgg	tcg	ctg	agc	acg	ggc	tcg	tcg	ccg	cgc	ggg	tcc	gac	
Thr	Thr	Pro	Arg	Ser	Leu	Ser	Thr	Gly	Ser	Ser	Pro	Arg	Gly	Ser	Asp	
														30		
gac	cg	agc	tcc	gac	gac	ggg	gag	gag	ctg	gtc	gag	gtc	acg	ctc	gac	
Asp	Arg	Ser	Ser	Asp	Asp	Gly	Glu	Glu	Leu	Val	Glu	Val	Thr	Leu	Asp	
													35	40	45	
ctg	cag	gac	gac	acc	att	gtg	ctt	cg	agc	gtc	gag	ccc	g	g	g	
Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala	Ala	
													50	55	60	
g	cg	g	cg	g	gg	gt	gg	g	cg	gg	g	cg	tc	g	gg	
Ala	Ala	Ala	Ala	Gly	Val	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Arg	
													65	70	75	80
gg	g	g	ct	ac	gg	gg	tc	tc	tc	tc	tc	cg	tc	gg	gg	
Gly	Glu	Leu	Thr	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Arg	Ser	Arg	Ser	Ser	
													85	90	95	
cc	tc	at	cg	gg	ag	ag	tc	tc	ca	cg	ct	tc	tc	ca	g	
Pro	Ser	Ile	Arg	Arg	Ser	Ser	Ser	His	Arg	Leu	Leu	Gln	Phe	Ser	Gln	
													100	105	110	
g	at	cg	g	gg	gg	at	gg	cc	gg	ca	tt	tc	cg	ca	g	
Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	
													115	120	125	
ct	ac	aa	cg	tt	gg	cg	cg	ac	ca	cg	aa	cg	ca	cg	cg	
Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	
													130	135	140	
cc	tc	gg	ct	gg	tc	gg	cc									
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	
													145	150	155	160
cg	cg	cag	ct	gac	cg	aca	cg	tcc	gg	cc	cac	aag	cg	ct	cg	
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg	
													165	170	175	
gg	ct	cg	tt	at	ag	ag	aa	gg	aa	aa	gg	tgg	at	g	g	
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu	
													180	185	190	

gtg cag gcc aac ttc gac cgc ctc gcc cgc gac ggc tac ctc tcc cgc	624
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg	
195 200 205	
tcc gac ttc gcc gaa tgc atc ggg atg acg gaa tcg aag gag ttc gcg	672
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala	
210 215 220	
ctc gag ctg ttc gac acg ctg agc cgg cga cga cag atg aag gtg gac	720
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Arg Gln Met Lys Val Asp	
225 230 235 240	
acg att aac aag gat gaa ctc cgc gag atc tgg cag cag atc acc gat	768
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp	
245 250 255	
aac agc ttc gac tcc cgt ctc caa atc ttc gaa atg gtg gat aag	816
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys	
260 265 270	
aac gcg gac ggc cg att acg gag ggc gag gtg aaa gag att att atg	864
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met	
275 280 285	
ttg agc gcg tct gcc aat aaa ctg tcg agg ctt aag gag caa gca gaa	912
Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu	
290 295 300	
gag tac gcc gct ttg atc atg gag gag ctt gat cct gaa ggg ctc ggc	960
Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Gly Leu Gly	
305 310 315 320	
tac att gag cta tgg caa ttg gag aca ctt ctg ttg cag aaa gat acc	1008
Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr	
325 330 335	
tat atg aac tat agt cag gcc ctt agt tac aca agc caa gca ctg agc	1056
Tyr Met Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser	
340 345 350	
cag aat ctt gca ggg cta agg aag aag agt tca atc cgc aaa ata agc	1104
Gln Asn Leu Ala Gly Leu Arg Lys Lys Ser Ser Ile Arg Lys Ile Ser	
355 360 365	
acc tct tta agc tac tat ttc gag gac aac tgg aaa cgt tta tgg gtg	1152
Thr Ser Leu Ser Tyr Tyr Phe Glu Asp Asn Trp Lys Arg Leu Trp Val	
370 375 380	
ctt gca ttg tgg att ggg ata atg gct gga ctg ttc acc tgg aaa ttc	1200
Leu Ala Leu Trp Ile Gly Ile Met Ala Gly Leu Phe Thr Trp Lys Phe	
385 390 395 400	
atg cag tat cgt aac cga tat gtc ttt gat gtg atg ggc tac tgt gtc	1248
Met Gln Tyr Arg Asn Arg Tyr Val Phe Asp Val Met Gly Tyr Cys Val	
405 410 415	
aca aca gca aaa gga gct gct gaa acc cta aag ctg aat atg gca att	1296
Thr Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu Asn Met Ala Ile	
420 425 430	
atc ctc ctg cca gta tgc cgt aac acc att act tgg ttg cga agt aca	1344
Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser Thr	
435 440 445	
agg gct gca cgg gca cta cct ttt gat gac aac atc aac ttc cac aag	1392
Arg Ala Ala Arg Ala Leu Pro Phe Asp Asp Asn Ile Asn Phe His Lys	
450 455 460	
act att gca gca gca att gtg gtt ggt ata atc ctc cat gca ggg aac	1440
Thr Ile Ala Ala Ala Ile Val Val Gly Ile Ile Leu His Ala Gly Asn	
465 470 475 480	
cac ctt gta tgc gat ttt cca cgg tta ata aaa tca tca gat gag aag	1488
His Leu Val Cys Asp Phe Pro Arg Leu Ile Lys Ser Ser Asp Glu Lys	
485 490 495	
tat gct cct ttg ggc cag tat ttt ggg gaa ata aag cca aca tat ttt	1536
Tyr Ala Pro Leu Gly Gln Tyr Phe Gly Glu Ile Lys Pro Thr Tyr Phe	
500 505 510	
aca ttg gtc aaa gga gtg gag ggc atc act ggg gta atc atg gtt gta	1584

Thr	Leu	Val	Lys	Gly	Val	Glu	Gly	Ile	Thr	Gly	Val	Ile	Met	Val	Val	
515					520							525				
tgc	atg	ata	att	gct	ttt	act	cta	gca	acc	cg	tgg	ttc	cgc	cgt	agc	1632
Cys	Met	Ile	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser	
530					535					540						
ttg	gtt	aag	ctt	cca	agg	cca	ttt	gac	aaa	ctg	act	ggc	ttc	aat	gcc	1680
Leu	Val	Lys	Leu	Pro	Arg	Pro	Phe	Asp	Lys	Leu	Thr	Gly	Phe	Asn	Ala	
545					550					555				560		
ttt	tgg	tat	tct	cat	cat	ctg	ttc	atc	att	gtg	tat	atc	gcf	ctc	att	1728
Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ile	Ala	Leu	Ile	
565					570					575						
gtt	cat	gga	gag	tgt	cta	tac	ctt	att	cat	gtc	tgg	tac	aga	aga	acg	1776
Val	His	Gly	Glu	Cys	Leu	Tyr	Leu	Ile	His	Val	Trp	Tyr	Arg	Arg	Thr	
580					585					590						
aca	tgg	atg	tat	ctt	tca	gtg	cct	gtt	tgc	ttg	tat	gta	ggg	gag	agg	1824
Thr	Trp	Met	Tyr	Leu	Ser	Val	Pro	Val	Cys	Leu	Tyr	Val	Gly	Glu	Arg	
595					600					605						
att	cta	agg	ttc	ttc	agg	tct	ggc	agt	tat	tct	gtc	cg	cta	ttg	aag	1872
Ile	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Ser	Tyr	Ser	Val	Arg	Leu	Leu	Lys	
610					615					620						
gtg	gcc	ata	tat	cca	ggt	aat	gtt	ttg	aca	ctg	caa	atg	tcc	aag	cct	1920
Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	Lys	Pro	
625					630					635				640		
ccc	acg	tcc	cgt	tac	aag	agt	gga	caa	tat	atg	ttt	gtt	caa	tgt	cca	1968
Pro	Thr	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro	
645					650					655						
gca	gtg	tct	ccc	ttt	gaa	tgg	cat	ccc	ttc	tca	att	act	tca	gca	cct	2016
Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	
660					665					670						
ggg	gat	gac	tac	ctc	agc	att	cat	gtt	cga	caa	ctt	ggt	gat	tgg	aca	2064
Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Val	Arg	Gln	Leu	Gly	Asp	Trp	Thr	
675					680					685						
cga	gaa	ctc	aag	aga	gta	ttt	gct	gca	gct	tgt	gag	ccc	cca	gcg	ggt	2112
Arg	Glu	Leu	Lys	Arg	Val	Phe	Ala	Ala	Ala	Cys	Glu	Pro	Pro	Ala	Gly	
690					695					700						
ggt	aaa	agc	ggc	ctt	ctt	agg	gca	gat	gag	aca	act	aag	aaa	atc	tta	2160
Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Thr	Thr	Lys	Lys	Ile	Leu	
705					710					715				720		
ccc	aag	ctt	ctg	att	gat	gga	ccg	tat	ggt	tct	cct	gct	cag	gat	tac	2208
Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ser	Pro	Ala	Gln	Asp	Tyr	
725					730					735						
agc	aag	tat	gat	gtt	tta	tta	ctt	gtt	gga	tta	gga	att	ggt	gca	aca	2256
Ser	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	
740					745					750						
ccc	ttt	att	agc	ata	tta	aaa	gat	ctt	ctg	aat	aac	atc	atc	aaa	atg	2304
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Ile	Lys	Met	
755					760					765						
gag	gaa	gag	gag	gat	gct	tct	act	gat	ctt	tat	cca	cca	atg	ggt	cg	2352
Glu	Glu	Glu	Glu	Asp	Ala	Ser	Thr	Asp	Leu	Tyr	Pro	Pro	Met	Gly	Arg	
770					775					780						
aat	aag	cca	cat	gtt	gat	ctg	ggc	aca	ctt	atg	acg	att	acc	tca	aga	2400
Asn	Lys	Pro	His	Val	Asp	Leu	Gly	Thr	Leu	Met	Thr	Ile	Thr	Ser	Arg	
785					790					795				800		
cca	aag	aag	atc	ttg	aag	acc	aca	aat	gct	tac	ttt	tac	tgg	gtg	aca	2448
Pro	Lys	Lys	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	
805					810					815						
cgt	gag	caa	ggc	tct	ttt	gat	tgg	ttc	aaa	gga	gtc	atg	aat	gaa	att	2496
Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile	
820					825					830						
gct	gac	ttg	gat	caa	agg	aat	atc	att	gag	atg	cac	aac	tac	cta	aca	2544
Ala	Asp	Leu	Asp	Gln	Arg	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	

835	840	845	
agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc			2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu			
850	855	860	
caa gct ctg aac cat gcc aag aat gga gtt gat att gtc tct ggg aca			2640
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr			
865	870	875	880
aaa gtc cgg aca cat ttt gca cga cca aat tgg aga aag gtc ctt tct			2688
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser			
885	890	895	
aaa att tcc tcc aag cat cca tat gcc aaa ata ggt gta ttc tac tgt			2736
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys			
900	905	910	
gga gct cca gtc ctg gca caa gaa cta agc aaa ctt tgc cat gaa ttc			2784
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe			
915	920	925	
aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga			2832
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe			
930	935	940	

<210> 4
 <211> 943
 <212> PRT
 <213> Oryza sativa

<400> 4			
Met Arg Gly Gly Ala Ser Ser Gly Pro Gln Arg Trp Gly Ser Ala Gly			
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Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp			
20	25	30	
Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp			
35	40	45	
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala			
50	55	60	
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Ala Ser Ala Arg			
65	70	75	80
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser			
85	90	95	
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln			
100	105	110	
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp			
115	120	125	
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala			
130	135	140	
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln			
145	150	155	160
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg			
165	170	175	
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu			
180	185	190	
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg			
195	200	205	
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala			
210	215	220	
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Arg Gln Met Lys Val Asp			
225	230	235	240
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp			
245	250	255	
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys			
260	265	270	
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met			

275	280	285
Leu Ser Ala Ser Ala Asn Lys	Leu Ser Arg Leu Lys	Glu Gln Ala Glu
290	295	300
Glu Tyr Ala Ala Leu Ile Met	Glu Glu Leu Asp	Pro Glu Gly Leu Gly
305	310	315
Tyr Ile Glu Leu Trp Gln Leu Glu Thr	Leu Leu Leu Gln Lys Asp	Thr
325	330	335
Tyr Met Asn Tyr Ser Gln Ala Leu Ser	Tyr Thr Ser Gln Ala Leu Ser	
340	345	350
Gln Asn Leu Ala Gly Leu Arg Lys	Lys Ser Ser Ile Arg Lys Ile Ser	
355	360	365
Thr Ser Leu Ser Tyr Tyr Phe	Glu Asp Asn Trp Lys Arg	Leu Trp Val
370	375	380
Leu Ala Leu Trp Ile Gly Ile Met Ala Gly	Leu Phe Thr Trp Lys Phe	
385	390	395
Met Gln Tyr Arg Asn Arg Tyr Val Phe	Asp Val Met Gly Tyr Cys	Val
405	410	415
Thr Thr Ala Lys Gly Ala Ala Glu	Thr Leu Lys Leu Asn Met Ala Ile	
420	425	430
Ile Leu Leu Pro Val Cys Arg Asn	Thr Ile Thr Trp Leu Arg Ser Thr	
435	440	445
Arg Ala Ala Arg Ala Leu Pro Phe Asp Asp Asn	Ile Asn Phe His Lys	
450	455	460
Thr Ile Ala Ala Ala Ile Val Val Gly	Ile Ile Leu His Ala Gly Asn	
465	470	475
His Leu Val Cys Asp Phe Pro Arg Leu	Ile Lys Ser Ser Asp Glu Lys	
485	490	495
Tyr Ala Pro Leu Gly Gln Tyr Phe	Gly Glu Ile Lys Pro Thr Tyr Phe	
500	505	510
Thr Leu Val Lys Gly Val Glu	Gly Ile Thr Gly Val Ile Met Val Val	
515	520	525
Cys Met Ile Ile Ala Phe	Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser	
530	535	540
Leu Val Lys Leu Pro Arg Pro Phe Asp Lys	Leu Thr Gly Phe Asn Ala	
545	550	555
Phe Trp Tyr Ser His His Leu Phe	Ile Ile Val Tyr Ile Ala Leu Ile	
565	570	575
Val His Gly Glu Cys Leu Tyr Leu Ile His	Val Val Trp Tyr Arg Arg Thr	
580	585	590
Thr Trp Met Tyr Leu Ser Val Pro Val Cys	Leu Tyr Val Gly Glu Arg	
595	600	605
Ile Leu Arg Phe Phe Arg Ser Gly Ser	Tyr Ser Val Arg Leu Leu Lys	
610	615	620
Val Ala Ile Tyr Pro Gly Asn Val	Leu Thr Leu Gln Met Ser Lys Pro	
625	630	635
Pro Thr Phe Arg Tyr Lys Ser Gly	Gln Tyr Met Phe Val Gln Cys Pro	
645	650	655
Ala Val Ser Pro Phe Glu Trp His	Pro Phe Ser Ile Thr Ser Ala Pro	
660	665	670
Gly Asp Asp Tyr Leu Ser Ile His	Val Arg Gln Leu Gly Asp Trp Thr	
675	680	685
Arg Glu Leu Lys Arg Val Phe	Ala Ala Ala Cys Glu Pro Pro Ala Gly	
690	695	700
Gly Lys Ser Gly Leu Leu Arg Ala Asp	Glu Thr Thr Lys Lys Ile Leu	
705	710	715
Pro Lys Leu Leu Ile Asp Gly Pro	Tyr Gly Ser Pro Ala Gln Asp Tyr	
725	730	735
Ser Lys Tyr Asp Val Leu Leu Val	Gly Leu Gly Ile Gly Ala Thr	
740	745	750
Pro Phe Ile Ser Ile Leu Lys Asp	Leu Leu Asn Asn Ile Ile Lys Met	
755	760	765

Glu	Glu	Glu	Glu	Asp	Ala	Ser	Thr	Asp	Leu	Tyr	Pro	Pro	Met	Gly	Arg
770						775					780				
Asn	Lys	Pro	His	Val	Asp	Leu	Gly	Thr	Leu	Met	Thr	Ile	Thr	Ser	Arg
785					790					795					800
Pro	Lys	Lys	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr
						805			810						815
Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile
						820			825						830
Ala	Asp	Leu	Asp	Gln	Arg	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr
						835			840						845
Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu
						850			855						860
Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr
						865			870			875			880
Lys	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Leu	Ser
						885				890					895
Lys	Ile	Ser	Ser	Lys	His	Pro	Tyr	Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys
						900			905						910
Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu	Leu	Ser	Lys	Leu	Cys	His	Glu	Phe
						915			920						925
Asn	Gly	Lys	Cys	Thr	Thr	Lys	Phe	Glu	Phe	His	Lys	Glu	His	Phe	
						930			935						940

<210> 5
<211> 2889
<212> DNA
<213> Nicotiana tabacum

<220>
<221> CDS
<222> (1)..(2886)
<223> coding for NADPH oxidase

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Met	Arg	Gly	Leu	Pro	Gly	His	Glu	Arg	Arg	Trp	Thr	Ser	Asp	Thr	Val
1			5							10					15
tct	tcc	gac	aag	gat	ttt	agt	ggt	gaa	tta	tcg	ccg	gga	gct	gat	tcc
Ser	Ser	Asp	Lys	Asp	Phe	Ser	Gly	Glu	Leu	Ser	Pro	Gly	Ala	Asp	Ser
						20			25						30
ggc	tat	aat	tcc	ggt	ttt	gct	tcc	gag	gag	ttt	gtt	gaa	gtc	acg	ctt
Gly	Tyr	Asn	Ser	Gly	Phe	Ala	Ser	Glu	Glu	Phe	Val	Glu	Val	Thr	Leu
						35			40						45
gat	ctt	cag	gat	gat	acc	att	att	cta	cg	agc	gtt	gaa	ccg	gct	
Asp	Leu	Gln	Asp	Asp	Asp	Thr	Ile	Ile	Leu	Arg	Ser	Val	Glu	Pro	Ala
						50			55						60
act	gtg	att	aac	att	gac	gct	cct	gat	ctt	ccc	gcc	gga	gtc	ggt	att
Thr	Val	Ile	Asn	Ile	Asp	Ala	Pro	Asp	Leu	Pro	Ala	Gly	Val	Gly	Ile
						65			70			75			80
tcc	gga	gtt	tca	att	gaa	act	ccg	acg	tca	gca	tcg	gtg	tcg	gaa	tct
Ser	Gly	Val	Ser	Ile	Glu	Thr	Pro	Thr	Ser	Ala	Ser	Val	Ser	Glu	Ser
						85			90						95
cga	tcg	ccg	acg	atc	cg	cg	agt	tca	tct	agt	aaa	ctt	cgt	cag	ttt
Arg	Ser	Pro	Thr	Ile	Arg	Arg	Ser	Ser	Ser	Ser	Lys	Leu	Arg	Gln	Phe
						100			105						110
tca	cag	gag	ttg	aaa	gct	gag	g	g	gtt	g	aaa	g	agg	c	tca
Ser	Gln	Glu	Leu	Lys	Ala	Glu	Ala	Val	Ala	Lys	Ala	Arg	Gln	Phe	Ser
						115			120						125
caa	gag	ctg	aag	g	g	g	tta	agg	aga	t	tc	tgg	agc	cat	ggg
Gln	Glu	Leu	Lys	Ala	Glu	Leu	Arg	Arg	Phe	Ser	Trp	Ser	His	Gly	His
						130			135						140

gct tct cgc gcg ttt tcg ccc tcg tcg ttt ttt caa aac gcc gtc gtt	480
Ala Ser Arg Ala Phe Ser Pro Ser Ser Phe Phe Gln Asn Ala Val Val	
145 150 155 160	
gga aca ggt aac ggc gtc gac tcg gct tta gcg gca cgt gca tta cgt	528
Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu Arg	
165 170 175	
cgg caa cgc gcg cag ctt gat cgg act cgt tcc agc gcc cat aga gct	576
Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Arg Ala	
180 185 190	
ctt cgt aga ctc aaa ttc att agc aat aac aaa acc aat gga tgg aat	624
Leu Arg Arg Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp Asn	
195 200 205	
gaa gtt gaa aac aat ttc tca aag ctc gct aaa gac ggt tat ctt tac	672
Glu Val Glu Asn Asn Phe Ser Lys Leu Ala Lys Asp Gly Tyr Leu Tyr	
210 215 220	
cgt tcc gat ttc gca caa tgc ata ggt atg aag gat tcg aag gaa ttt	720
Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys Asp Ser Lys Glu Phe	
225 230 235 240	
gca ttg gaa tta ttt gat gct ttg agt aga aga aga tta aag gtt	768
Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys Val	
245 250 255	
gat aaa att agc aag gag gaa ttg tat gag tac tgg tct caa atc acc	816
Asp Lys Ile Ser Lys Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr	
260 265 270	
gat cag agt ttc gat tct cgg ctt cag atc tcc ttc gac atg gtg gac	864
Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Ser Phe Asp Met Val Asp	
275 280 285	
aag aat gaa gat ggt cga att gct gaa gag gaa gta aaa gag atc atc	912
Lys Asn Glu Asp Gly Arg Ile Ala Glu Glu Glu Val Lys Glu Ile Ile	
290 295 300	
atg cta agt gca tct gca aac aag tta tca aga tta aaa gaa caa gca	960
Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala	
305 310 315 320	
gag gag tat gca gct tta atc atg gaa gaa tta gat cct gaa aga ctc	1008
Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Arg Leu	
325 330 335	
ggc tac att gag cta tgg cag ctg gaa aca ctt ctc ctc caa aag gac	1056
Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp	
340 345 350	
act tac ctc aac tac agt caa gca cta agt tac acg agc caa gcc ttg	1104
Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu	
355 360 365	
agc caa aac ctt cac gga tta agg aag aaa agc cca ata aaa aga atg	1152
Ser Gln Asn Leu His Gly Leu Arg Lys Lys Ser Pro Ile Lys Arg Met	
370 375 380	
agc aca aaa ctt gtc tat tca ttg caa gaa aac tgg aag aga att tgg	1200
Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp	
385 390 395 400	
gtt ctc act tta ttg att ttg ata atg att ggg ctt ttt ctt tgg aag	1248
Val Leu Thr Leu Trp Ile Leu Ile Met Ile Gly Leu Phe Leu Trp Lys	
405 410 415	
ttc tat cag tac aaa aac aag agt gca ttc cgt gtc atg ggt tat tgc	1296
Phe Tyr Gln Tyr Lys Asn Lys Ser Ala Phe Arg Val Met Gly Tyr Cys	
420 425 430	
ctt gtc acg gct aag ggc gct gct gag act ctc aag ttc aac atg gct	1344
Leu Val Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Phe Asn Met Ala	
435 440 445	
ctt ata tta ttg cca gta tgc aga aac act att aca tgg ctc agg tcc	1392
Leu Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser	
450 455 460	
acc aag ttg agc cat ttt gta ccc ttt gac gac aac atc aac ttt cac	1440

Thr	Lys	Leu	Ser	His	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	
465					470					475					480	
aag	act	gtc	gct	gca	gcc	att	gtc	act	ggt	atc	ata	ctc	cat	gct	ggt	1488
Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala	Gly	
						485				490				495		
aac	cat	ctt	gta	tgt	gat	ttc	cca	agg	ctt	ata	cat	gca	gat	gat	caa	1536
Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	His	Ala	Asp	Asp	Gln	
						500			505				510			
gat	tat	caa	agt	ttt	ttg	tcg	aat	gat	ttt	ggc	caa	agt	aag	cct	gga	1584
Asp	Tyr	Gln	Ser	Phe	Leu	Ser	Asn	Asp	Phe	Gly	Gln	Ser	Lys	Pro	Gly	
						515			520			525				
tac	ata	gac	ctt	gtt	aaa	gga	gtt	gag	ggt	gtg	acg	gga	ata	ata	atg	1632
Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	Ile	Met	
						530			535			540				
gta	atc	ctt	atg	gcc	att	gct	ttc	act	ctt	gct	aca	cga	tgg	ttt	aga	1680
Val	Ile	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	
						545			550			555			560	
cg	ggc	ctc	att	aag	ttg	ccc	aaa	cct	ttt	gat	aga	ctc	act	ggc	ttc	1728
Arg	Ser	Leu	Ile	Lys	Leu	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly	Phe	
						565			570						575	
aat	gca	ttc	tgg	tat	tca	cac	cac	ctt	gtc	att	gtc	tac	atc	cta		1776
Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Val	Ile	Val	Tyr	Ile	Leu	
						580			585			590				
ctg	atc	atc	cat	ggc	acg	ttc	ctc	ttc	ctt	gtg	cat	aaa	tgg	tac	tcc	1824
Leu	Ile	Ile	His	Gly	Thr	Phe	Leu	Phe	Leu	Val	His	Lys	Trp	Tyr	Ser	
						595			600			605				
aag	acg	acg	tgg	atg	tat	cta	gca	gtt	cct	gtg	ctt	ctc	tac	gca	ggg	1872
Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ala	Val	Pro	Val	Leu	Leu	Tyr	Ala	Gly	
						610			615			620				
gaa	aga	act	ctt	aga	ttc	ttc	cgg	tca	ggc	ttg	tac	act	gtc	cgg	ttt	1920
Glu	Arg	Thr	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Thr	Val	Arg	Leu	
						625			630			635			640	
ctg	aaa	gta	gca	ata	tat	cct	gga	aat	gtc	ctc	act	cta	caa	atg	tct	1968
Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	
						645			650			655				
aag	cct	cct	caa	ttt	cga	tac	aaa	agt	gga	caa	tat	atg	ttt	gtc	cag	2016
Lys	Pro	Pro	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	
						660			665			670				
tgt	cca	gct	gtt	tct	cca	ttc	gag	tgg	cat	cca	ttt	tcc	att	act	tca	2064
Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	
						675			680			685				
gct	cct	ggg	gat	gac	tac	ttg	agc	att	cac	atc	cgg	caa	ctt	gg	gac	2112
Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	Gly	Asp	
						690			695			700				
tgg	act	caa	gaa	ctc	aag	cgg	gtc	ttt	tct	gag	gct	tgc	gag	cgg	cca	2160
Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	Arg	Pro	
						705			710			715			720	
gag	gct	gga	aag	agt	ggc	ctg	ctc	aga	gct	gac	gaa	aac	act	aag	aaa	2208
Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	Lys	Lys	
						725			730			735				
agt	ttg	cca	aag	cta	tta	ata	gat	gga	cct	tac	gga	gct	cca	gca	caa	2256
Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	
						740			745			750				
gat	tac	cga	aaa	tat	gat	gtc	ttg	ctg	ttt	ggt	ctt	ggc	att	gga		2304
Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	
						755			760			765				
gca	acg	ccg	ttc	ata	agt	atc	ctg	aaa	gac	ttg	ctc	gtt	aac	atc	gtg	2352
Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Val	Asn	Ile	Val	
						770			775			780				
aaa	atg	gag	gag	caa	gca	gat	tta	gcc	tca	gat	ttc	agt	ggg	aac	tca	2400
Lys	Met	Glu	Glu	Gln	Ala	Asp	Leu	Ala	Ser	Asp	Phe	Ser	Gly	Asn	Ser	

785	790	795	800	
gac atg agc gtt gcg aca agt gaa caa cca gct ctc aac aag att tct				2448
Asp Met Ser Val Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser				
805	810	815		
ctg aaa agg aga aag agc act cta aga acc aca aat gca tat ttt tat				2496
Leu Lys Arg Arg Lys Ser Thr Leu Arg Thr Thr Asn Ala Tyr Phe Tyr				
820	825	830		
tgg gtg acc cgg gag caa gga tca ttt gat tgg ttc aaa ggc gtt atg				2544
Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met				
835	840	845		
aac gaa gtg gct gaa ctt gat caa agg ggg gtc atc gag atg cat aac				2592
Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn				
850	855	860		
tac ttg acg agt gtt tat gag gaa ggg gat gct cgt tca gct ctc att				2640
Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile				
865	870	875	880	
acc atg gtc cag gca ctt aac cat gct aag aat ggg gtt gat att gta				2688
Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val				
885	890	895		
tca ggc acc agg gtg agg aca cat ttt gct agg cca aat tgg aag aaa				2736
Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys				
900	905	910		
gta ttt tcc aag acc tta acc aag cat gca aat gca aga ata ggg gtt				2784
Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val				
915	920	925		
ttc tac tgt ggt gca ccc gta tta gca aaa gaa ctc agc aaa ctc tgc				2832
Phe Tyr Cys Gly Ala Pro Val Leu Ala Lys Glu Leu Ser Lys Leu Cys				
930	935	940		
aaa gag tat aat caa aag ggt gca aca aag ttc gag ttt cac aaa gaa				2880
Lys Glu Tyr Asn Gln Lys Gly Ala Thr Lys Phe Glu Phe His Lys Glu				
945	950	955	960	
cat ttt tag				2889
His Phe				

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<212> PRT
<213> Nicotiana tabacum

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Ser Ser Asp Lys Asp Phe Ser Gly Glu Leu Ser Pro Gly Ala Asp Ser				
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Gly Tyr Asn Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Thr Leu				
35	40	45		
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala				
50	55	60		
Thr Val Ile Asn Ile Asp Ala Pro Asp Leu Pro Ala Gly Val Gly Ile				
65	70	75	80	
Ser Gly Val Ser Ile Glu Thr Pro Thr Ser Ala Ser Val Ser Glu Ser				
85	90	95		
Arg Ser Pro Thr Ile Arg Arg Ser Ser Ser Ser Lys Leu Arg Gln Phe				
100	105	110		
Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Arg Gln Phe Ser				
115	120	125		
Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly His				
130	135	140		
Ala Ser Arg Ala Phe Ser Pro Ser Ser Phe Phe Gln Asn Ala Val Val				
145	150	155	160	
Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Arg Ala Leu Arg				

165	170	175
Arg Gln Arg Ala Gln Leu Asp Arg	Thr Arg Ser Ser Ala His	Arg Ala
180	185	190
Leu Arg Arg Leu Lys Phe Ile Ser Asn Asn Lys	Thr Asn Gly Trp Asn	
195	200	205
Glu Val Glu Asn Asn Phe Ser Lys Leu Ala Lys	Asp Gly Tyr Leu Tyr	
210	215	220
Arg Ser Asp Phe Ala Gln Cys Ile Gly Met	Lys Asp Ser Lys Glu	Phe
225	230	240
Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg	Arg Arg Arg Leu Lys Val	
245	250	255
Asp Lys Ile Ser Lys Glu Glu Leu Tyr	Glu Tyr Trp Ser Gln Ile Thr	
260	265	270
Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Ser	Phe Asp Met Val Asp	
275	280	285
Lys Asn Glu Asp Gly Arg Ile Ala Glu Glu Glu	Val Lys Glu Ile Ile	
290	295	300
Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg	Leu Lys Glu Gln Ala	
305	310	320
Glu Glu Tyr Ala Ala Leu Ile Met	Glu Leu Asp Pro Glu Arg Leu	
325	330	335
Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr	Leu Leu Leu Gln Lys Asp	
340	345	350
Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr	Thr Ser Gln Ala Leu	
355	360	365
Ser Gln Asn Leu His Gly Leu Arg Lys Lys	Ser Pro Ile Lys Arg Met	
370	375	380
Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn	Trp Lys Arg Ile Trp	
385	390	400
Val Leu Thr Leu Trp Ile Leu Ile Met	Ile Gly Leu Phe Leu Trp Lys	
405	410	415
Phe Tyr Gln Tyr Lys Asn Lys Ser Ala Phe Arg	Val Met Gly Tyr Cys	
420	425	430
Leu Val Thr Ala Lys Gly Ala Ala Glu Thr	Leu Lys Phe Asn Met Ala	
435	440	445
Leu Ile Leu Leu Pro Val Cys Arg Asn Thr	Ile Thr Trp Leu Arg Ser	
450	455	460
Thr Lys Leu Ser His Phe Val Pro Phe Asp	Asp Asn Ile Asn Phe His	
465	470	480
Lys Thr Val Ala Ala Ile Val Thr Gly	Ile Ile Leu His Ala Gly	
485	490	495
Asn His Leu Val Cys Asp Phe Pro Arg	Leu Ile His Ala Asp Asp Gln	
500	505	510
Asp Tyr Gln Ser Phe Leu Ser Asn Asp Phe	Gly Gln Ser Lys Pro Gly	
515	520	525
Tyr Ile Asp Leu Val Lys Gly Val Glu	Gly Val Thr Gly Ile Ile Met	
530	535	540
Val Ile Leu Met Ala Ile Ala Phe Thr	Leu Ala Thr Arg Trp Phe Arg	
545	550	560
Arg Ser Leu Ile Lys Leu Pro Lys Pro	Phe Asp Arg Leu Thr Gly Phe	
565	570	575
Asn Ala Phe Trp Tyr Ser His His	Leu Val Ile Val Tyr Ile Leu	
580	585	590
Leu Ile Ile His Gly Thr Phe	Leu Phe Leu Val His Lys Trp Tyr Ser	
595	600	605
Lys Thr Thr Trp Met Tyr Leu Ala Val Pro	Val Leu Tyr Ala Gly	
610	615	620
Glu Arg Thr Leu Arg Phe Phe Arg Ser	Gly Leu Tyr Thr Val Arg Leu	
625	630	640
Leu Lys Val Ala Ile Tyr Pro Gly Asn	Val Leu Thr Leu Gln Met Ser	
645	650	655

Lys Pro Pro Gln Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln
 660 665 670
 Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser
 675 680 685
 Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu Gly Asp
 690 695 700
 Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu Arg Pro
 705 710 715 720
 Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys Lys
 725 730 735
 Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln
 740 745 750
 Asp Tyr Arg Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly
 755 760 765
 Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Val Asn Ile Val
 770 775 780
 Lys Met Glu Glu Gln Ala Asp Leu Ala Ser Asp Phe Ser Gly Asn Ser
 785 790 795 800
 Asp Met Ser Val Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser
 805 810 815
 Leu Lys Arg Arg Lys Ser Thr Leu Arg Thr Thr Asn Ala Tyr Phe Tyr
 820 825 830
 Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met
 835 840 845
 Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn
 850 855 860
 Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile
 865 870 875 880
 Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val
 885 890 895
 Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys
 900 905 910
 Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val
 915 920 925
 Phe Tyr Cys Gly Ala Pro Val Leu Ala Lys Glu Leu Ser Lys Leu Cys
 930 935 940
 Lys Glu Tyr Asn Gln Lys Gly Ala Thr Lys Phe Glu Phe His Lys Glu
 945 950 955 960
 His Phe

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<220>
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 tattttatcta ttgtgcttg atttggaca a atg agg ggt tta cct ggg cat 112
 Met Arg Gly Leu Pro Gly His
 1 5
 gaa cgc cgg tgg acg tcg gat acg gta tct tcc ggc aag gat tta agt 160
 Glu Arg Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser
 10 15 20
 ggt gag tca tcg ccg gga act gat tcc ggg aat att tcc ggt ttt gct 208
 Gly Glu Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala

25	30	35	
tcc gag gag ttt gtt gaa gtt ata ctt gat ctt	cag gat gat gat acg		256
Ser Glu Glu Phe Val Glu Val Ile Leu Asp Leu	Gln Asp Asp Asp Thr		
40	45	50	55
att att cta cgg agc gtt gaa ccg gct act gta	atc aac att gat gct		304
Ile Ile Leu Arg Ser Val Glu Pro Ala Thr Val	Ile Asn Ile Asp Ala		
60	65	70	
tct gat cct gct acc gga gtc ggt att ggt gga	gta tcg att gaa act		352
Ser Asp Pro Ala Thr Gly Val Gly Ile Gly	Gly Val Ser Ile Glu Thr		
75	80	85	
ccg gcg tcg ctg act tcg acg tcg gga act cga	tcg ccg acg atg cgt		400
Pro Ala Ser Leu Thr Ser Thr Ser Gly Thr Arg	Ser Pro Thr Met Arg		
90	95	100	
cgg agt aca tcg aat aaa tta cgt cag ttt tca	cag gag ttg aaa gct		448
Arg Ser Thr Ser Asn Lys Leu Arg Gln Phe Ser	Gln Glu Leu Lys Ala		
105	110	115	
gag gct gtc gcg aaa gcg aag cat ttc tcg caa	gag ctt aaa gcg gag		496
Glu Ala Val Ala Lys Ala Lys His Phe Ser Gln	Glu Leu Lys Ala Glu		
120	125	130	135
cta agg aga ttc tca tgg agc cat gga cat gcg	tct cgc act ttt tcg		544
Leu Arg Arg Phe Ser Trp Ser His Gly His Ala	Ser Arg Thr Phe Ser		
140	145	150	
ccg gcg tcg ttt ttc caa aac gcc gtc gtc ggt	aca ggc aac ggt gta		592
Pro Ala Ser Phe Phe Gln Asn Ala Val Val Gly	Gly Thr Gly Asn Gly Val		
155	160	165	
gat tcg gct tta gca gct cga gca tta cga cgg	cag cgc gct cag ctc		640
Asp Ser Ala Leu Ala Ala Arg Ala Leu Arg Arg	Gln Arg Ala Gln Leu		
170	175	180	
gat cgg act cgt tcc agc gct cac aag gct ctt	cgt gga ctc aaa ttc		688
Asp Arg Thr Arg Ser Ser Ala His Lys Ala Leu	Arg Gly Leu Lys Phe		
185	190	195	
atc agc aat aac aaa act aac gga tgg aat gaa	ggt gaa aac aat ttt		736
Ile Ser Asn Asn Lys Thr Asn Gly Trp Asn Glu	Val Glu Asn Asn Phe		
200	205	210	215
gct aag ctc gct aaa gac ggt tac ctt tat cgc	tcc gat ttc gca caa		784
Ala Lys Leu Ala Lys Asp Gly Tyr Leu Tyr Arg	Ser Asp Phe Ala Gln		
220	225	230	
tgc atc ggt atg aag gat tca aag gaa ttt gca	ttg gaa ttg ttt gat		832
Cys Ile Gly Met Lys Asp Ser Lys Glu Phe Ala	Leu Glu Leu Phe Asp		
235	240	245	
gct ttg agt aga aga aga ttg aag gtt gat aag	att agc aaa gag		880
Ala Leu Ser Arg Arg Arg Leu Lys Val Asp Lys	Ile Ser Lys Glu		
250	255	260	
gaa ttg tat gag tat tgg tct caa atc acc gat	cag agt ttc gat tct		928
Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr Asp	Gln Ser Phe Asp Ser		
265	270	275	
ccg ctt cag atc ttc gac atg gtg gac aag aat	gaa gat ggt cga		976
Arg Leu Gln Ile Phe Phe Asp Met Val Asp Lys	Asn Glu Asp Gly Arg		
280	285	290	295
att ggt gaa gaa gaa gta aaa gag atc atc atg	cta agt gcc tct gca		1024
Ile Gly Glu Glu Val Lys Glu Ile Ile Met Leu	Ser Ala Ser Ala		
300	305	310	
aac aaa tta tca aga tta aaa gaa caa gca gag	gag tat gca gct ctg		1072
Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu	Tyr Ala Ala Leu		
315	320	325	
atc atg gaa gaa tta gat cct gaa aga ctt ggc	tac att gag cta tgg		1120
Ile Met Glu Glu Leu Asp Pro Glu Arg Leu Gly	Tyr Ile Glu Leu Trp		
330	335	340	
cag ctg gaa acg ctt ctc ctc caa aag gac act	tac ctc aac tac agt		1168
Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr	Tyr Tyr Leu Asn Tyr Ser		
345	350	355	

caa gca cta agc tac aca agc caa gct ttg agc caa aac ctg caa ggg Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser Gln Asn Leu Gln Gly 360 365 370 375	1216
ttg agg aag aga agc cca ata aga aga atg agc aca aaa ctt gtc tat Leu Arg Lys Arg Ser Pro Ile Arg Arg Met Ser Thr Lys Leu Val Tyr 380 385 390	1264
tca ctg caa gag aat tgg aag aga att tgg gtt ctg gtc ttg tgg att Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp Val Leu Val Leu Trp Ile 395 400 405	1312
ttg ata atg att gga ctt ttt ctt tgg aag ttc tat ctg tac aaa cag Leu Ile Met Ile Gly Leu Phe Leu Trp Lys Phe Tyr Leu Tyr Lys Gln 410 415 420	1360
aaa agt gca ttt caa gtt atg ggt tat tgc ctt cta aca gct aag ggt Lys Ser Ala Phe Gln Val Met Gly Tyr Cys Leu Leu Thr Ala Lys Gly 425 430 435	1408
gct gct gag act cta aag ttc aac atg gct ttg ata ttg ttg cca gtt Ala Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Leu Pro Val 440 445 450 455	1456
tgc agg aac acc att aca ttc ctc agg tct act aaa ttg agt tgt ttt Cys Arg Asn Thr Ile Thr Phe Leu Arg Ser Thr Lys Leu Ser Cys Phe 460 465 470	1504
gta ccc ttt gat gac aac atc aac ttc cac aag act gtt gct gca gcc Val Pro Phe Asp Asp Asn Ile Asn Phe His Lys Thr Val Ala Ala Ala 475 480 485	1552
att gtt act ggt atc ata ctc cat gcc ggt aat cat ctt gta tgt gat Ile Val Thr Gly Ile Ile Leu His Ala Gly Asn His Leu Val Cys Asp 490 495 500	1600
ttc cca aag ctt ata cat gca aat aat acg aat tat cag aaa tat ttg Phe Pro Lys Leu Ile His Ala Asn Asn Thr Asn Tyr Gln Lys Tyr Leu 505 510 515	1648
gtg aat gat ttt ggc cca agc cag cct cag tac ata gat ctt gtt aaa Val Asn Asp Phe Gly Pro Ser Gln Pro Gln Tyr Ile Asp Leu Val Lys 520 525 530 535	1696
gga gtg gag ggt gtg aca gga ata ata atg gta atc ctc atg gcc att Gly Val Glu Gly Val Thr Gly Ile Ile Met Val Ile Leu Met Ala Ile 540 545 550	1744
gct ttc act ctt gca acg cga tgg ttt agg cgg agc ctc att aag ttt Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser Leu Ile Lys Phe 555 560 565	1792
ccc aaa cct ttt gat aga ctc act ggt ttc aat gcg ttc tgg tac tcg Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr Ser 570 575 580	1840
cac cac ctt ctc atc att gtc tac atc gta ctg atc atc cat ggc aca His His Leu Leu Ile Ile Val Tyr Ile Val Leu Ile Ile His Gly Thr 585 590 595	1888
ttc ctc tac ctt gtg cat aac tgg tac tcc aaa acg aca tgg atg tat Phe Leu Tyr Leu Val His Asn Trp Tyr Ser Lys Thr Thr Trp Met Tyr 600 605 610 615	1936
cta gca gtt cct gta ctt ctc tac gca ggg gaa aga act ctt aga ttc Leu Ala Val Pro Val Leu Leu Tyr Ala Gly Glu Arg Thr Leu Arg Phe 620 625 630	1984
ttc cga tca ggc tta tat aca gtc cgg ctt cta aaa gta gca ata tat Phe Arg Ser Gly Leu Tyr Thr Val Arg Leu Leu Lys Val Ala Ile Tyr 635 640 645	2032
cct gga aat gtc ctt act ctg caa atg tct aag cct ccg caa ttt cga Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Pro Gln Phe Arg 650 655 660	2080
tac aag agt gga caa tat atg ttt gtc cag tgt cca gct gtt tct cca Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser Pro 665 670 675	2128
ttc gag tgg cat cca ttt tcc att act tca gct cct ggg gat gac tac	2176


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gtggggact gatagctttg ttgggtggAAC ttataatggg gctaaggGAAC tccttccAA 3530
aaatgtctat gtagtaacta ctttttcttt tgctttgtGA gtatTTTTG gggTATTtTA 3590
atatactact tattagataa gaggatagaa aatacgtgtA tatgcaattc ttattAGTAA 3650
agtttatctg tagtagttct ttaatctggA gaaaggtaCT atcaaaggAA atatctcatC 3710
qaaaaaaaaaa aaaaaaaaaaa aaa 3733
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<212> PRT
<213> *Solanum tuberosum*

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 Ser Ser Gly Lys Asp Leu Ser Gly Glu Ser Ser Pro Gly Thr Asp Ser
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 Gly Asn Ile Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Ile Leu
 35 40 45
 Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
 50 55 60
 Thr Val Ile Asn Ile Asp Ala Ser Asp Pro Ala Thr Gly Val Gly Ile
 65 70 75 80
 Gly Gly Val Ser Ile Glu Thr Pro Ala Ser Leu Thr Ser Thr Ser Gly
 85 90 95
 Thr Arg Ser Pro Thr Met Arg Arg Ser Thr Ser Asn Lys Leu Arg Gln
 100 105 110
 Phe Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Lys His Phe
 115 120 125
 Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly
 130 135 140
 His Ala Ser Arg Thr Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val
 145 150 155 160
 Val Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu
 165 170 175
 Arg Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Lys
 180 185 190
 Ala Leu Arg Gly Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp
 195 200 205
 Asn Glu Val Glu Asn Asn Phe Ala Lys Leu Ala Lys Asp Gly Tyr Leu
 210 215 220
 Tyr Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys Asp Ser Lys Glu
 225 230 235 240
 Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys
 245 250 255
 Val Asp Lys Ile Ser Lys Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile
 260 265 270
 Thr Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Asp Met Val
 275 280 285
 Asp Lys Asn Glu Asp Gly Arg Ile Gly Glu Glu Val Lys Glu Ile
 290 295 300
 Ile Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln
 305 310 315 320
 Ala Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Arg
 325 330 335
 Leu Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys
 340 345 350
 Asp Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala
 355 360 365
 Leu Ser Gln Asn Leu Gln Gly Leu Arg Lys Arg Ser Pro Ile Arg Arg
 370 375 380
 Met Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile

385	390	395	400																
Trp	Val	Leu	Val	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp				
																405	410	415	
Lys	Phe	Tyr	Leu	Tyr	Lys	Gln	Lys	Ser	Ala	Phe	Gln	Val	Met	Gly	Tyr				
																420	425	430	
Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met				
																435	440	445	
Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Phe	Leu	Arg				
																450	455	460	
Ser	Thr	Lys	Leu	Ser	Cys	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe				
																465	470	475	480
His	Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala				
																485	490	495	
Gly	Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Lys	Leu	Ile	His	Ala	Asn	Asn				
																500	505	510	
Thr	Asn	Tyr	Gln	Lys	Tyr	Leu	Val	Asn	Asp	Phe	Gly	Pro	Ser	Gln	Pro				
																515	520	525	
Gln	Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	Ile				
																530	535	540	
Met	Val	Ile	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe				
																545	550	555	560
Arg	Arg	Ser	Leu	Ile	Lys	Phe	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly				
																565	570	575	
Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Ile	Ile	Val	Tyr	Ile				
																580	585	590	
Val	Leu	Ile	Ile	His	Gly	Thr	Phe	Leu	Tyr	Leu	Val	His	Asn	Trp	Tyr				
																595	600	605	
Ser	Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ala	Val	Pro	Val	Leu	Leu	Tyr	Ala				
																610	615	620	
Gly	Glu	Arg	Thr	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Thr	Val	Arg				
																625	630	635	640
Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met				
																645	650	655	
Ser	Lys	Pro	Pro	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val				
																660	665	670	
Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr				
																675	680	685	
Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	Gly				
																690	695	700	
Asp	Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	Gln				
																705	710	715	720
Pro	Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	Lys				
																725	730	735	
Thr	Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala				
																740	745	750	
Gln	Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile				
																755	760	765	
Gly	Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Lys	Asn	Ile				
																770	775	780	
Val	Thr	Met	Glu	Glu	Gln	Ala	Asp	Leu	Val	Ser	Asp	Phe	Ser	Gly	Asn				
																785	790	795	800
Ser	Asp	Met	Ser	Ala	Ala	Thr	Ser	Glu	Gln	Pro	Ala	Leu	Asn	Lys	Ile				
																805	810	815	
Ser	Pro	Lys	Lys	Arg	Lys	Ser	Thr	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe				
																820	825	830	
Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val				
																835	840	845	
Met	Asn	Glu	Val	Ala	Glu	Leu	Asp	Gln	Arg	Gly	Val	Ile	Glu	Met	His				
																850	855	860	
Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu				
																865	870	875	880

Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile
 885 890 895
 Val Ser Gly Thr Ser Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg
 900 905 910
 Lys Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly
 915 920 925
 Val Phe Tyr Cys Gly Ala Pro Ile Leu Ala Lys Glu Leu Ser Lys Leu
 930 935 940
 Cys Lys Glu Phe Asn Gln Lys Gly Thr Thr Lys Phe Glu Phe His Lys
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 Glu His Phe

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 tttattgtca tttgatttgg gacag atg agg ggt tta cct ggg cat gaa cgc 172
 Met Arg Gly Leu Pro Gly His Glu Arg
 1 5
 cggtgg acgtcg gat acgtgtc tcc ggg aag gat tta agt ggt gag 220
 Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser Gly Glu
 10 15 20 25
 tca tcg ccg gga act gat tcc ggg aat att tcc ggt ttt gct tcg gag 268
 Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala Ser Glu
 30 35 40
 gag ttt gtt gaa gtt ata ctt gat ctt cag gat gat acg att att 316
 Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr Ile Ile
 45 50 55
 tta cgg agc gtt gaa ccg gct act gta atc aac att gat ggt tct gat 364
 Leu Arg Ser Val Glu Pro Ala Thr Val Ile Asn Ile Asp Gly Ser Asp
 60 65 70
 cct gct tcc gga gtc ggt att ggt gga gca tcg att gaa act ccg gcg 412
 Pro Ala Ser Gly Val Gly Ile Gly Gly Ala Ser Ile Glu Thr Pro Ala
 75 80 85
 tcg gtg acgtcg acgtcg gaa act cga tcg ccg atg atg cgt ccg agt 460
 Ser Val Thr Ser Thr Ser Glu Thr Arg Ser Pro Met Met Arg Arg Ser
 90 95 100 105
 aca tct aat aag ttt cgt cag ttt tca cag gag ttg aaa gct gag gct 508
 Thr Ser Asn Lys Phe Arg Gln Phe Ser Gln Glu Leu Lys Ala Glu Ala
 110 115 120
 gtt gcg aaa gcg aag cat ttc tcg caa gag ctt aaa gcg gag cta agg 556
 Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu Leu Arg
 125 130 135
 aga ttc tca tgg agc cat gga cat gcg tct cgt gct ttt tcg ccg gcg 604
 Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Ala Phe Ser Pro Ala
 140 145 150
 tcg ttt ttc caa aac gct gtc gtc gga aca ggc aac ggt gta gac tcg 652
 Ser Phe Phe Gln Asn Ala Val Val Gly Thr Gly Asn Gly Val Asp Ser
 155 160 165
 gct tta gcg gct cga gca tta cgt cgg cag cgt gct cag ctc gac cgg 700
 Ala Leu Ala Ala Arg Ala Leu Arg Arg Gln Arg Ala Gln Leu Asp Arg

170	175	180	185	
act cgt tcc agc gca cac aag gct ctt cgt	gga ctc aaa ttc atc agc			748
Thr Arg Ser Ser Ala His Lys Ala Leu Arg	Gly Leu Lys Phe Ile Ser			
190	195	200		
aat aac aaa act aac gga tgg aat gaa gtt gaa aac aat ttc gct aag				796
Asn Asn Lys Thr Asn Gly Trp Asn Glu Val	Glu Asn Asn Phe Ala Lys			
205	210	215		
ctc gct aaa gac ggt tac ctt tat cgt tcc gat ttc	gca caa tgc atc			844
Leu Ala Lys Asp Gly Tyr Leu Tyr Arg Ser Asp	Phe Ala Gln Cys Ile			
220	225	230		
ggt cag tac tca cgc cgg cga tca cta cag ttt	aat tat aga tta att			892
Gly Gln Tyr Ser Arg Arg Arg Ser Leu Gln Phe	Asn Tyr Arg Leu Ile			
235	240	245		
aca tta att ttg att aat tat ttg gtt aaa ggt	atg aag gat tca aag			940
Thr Leu Ile Leu Ile Asn Tyr Leu Val Lys	Gly Met Lys Asp Ser Lys			
250	255	260	265	
gaa ttt gcg ttg gaa ttg ttt gat gct tta agt	aga aga aga aga ttg			988
Glu Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser	Arg Arg Arg Arg Leu			
270	275	280		
aag gtt gat aag att agc caa gag gaa ttg tat	gag tat tgg tct caa			1036
Lys Val Asp Lys Ile Ser Gln Glu Glu Leu Tyr	Glu Tyr Trp Ser Gln			
285	290	295		
atc acc gat cag agt ttc gat tct cgg ctt cag	atc ttc ttc gac atg			1084
Ile Thr Asp Gln Ser Phe Asp Ser Arg Leu Gln	Ile Phe Phe Asp Met			
300	305	310		
gtg gac aag aat gaa gat ggt cga att ggt gaa	gaa gaa gta aaa gag			1132
Val Asp Lys Asn Glu Asp Gly Arg Ile Gly Glu	Glu Glu Val Lys Glu			
315	320	325		
atc atc atg cta agt gcc tct gca aac aaa tta	tca aga tta aaa gaa			1180
Ile Ile Met Leu Ser Ala Ser Ala Asn Lys	Leu Ser Arg Leu Lys Glu			
330	335	340	345	
caa gca gag gag tat gca gct ctg atc atg	gaa tta gat cct gaa			1228
Gln Ala Glu Glu Tyr Ala Ala Leu Ile Met	Glu Glu Leu Asp Pro Glu			
350	355	360		
aga ctt ggc tac att gag cta tgg cag ctg	gaa aca ctt ctc ctc caa			1276
Arg Leu Gly Tyr Ile Glu Leu Trp Gln Leu Glu	Thr Leu Leu Leu Gln			
365	370	375		
aag gac act tac ctc aac tac agt caa gca cta	agc tac aca agc caa			1324
Lys Asp Thr Tyr Leu Asn Tyr Ser Gln Ala Leu	Ser Tyr Thr Ser Gln			
380	385	390		
gct ttg agc caa aat ctg caa ggg ttg agg	aag aga agc cca ata aga			1372
Ala Leu Ser Gln Asn Leu Gln Gly Leu Arg	Lys Arg Ser Pro Ile Arg			
395	400	405		
aga atg agc aca aaa ctt gtc tat tca ctg	caa gag aat tgg aag aga			1420
Arg Met Ser Thr Lys Leu Val Tyr Ser Leu Gln	Glu Asn Trp Lys Arg			
410	415	420	425	
att tgg gtt ctg gtc ttg tgg att ttg ata	atg att gga ctt ttt ctt			1468
Ile Trp Val Leu Val Leu Trp Ile Leu Ile	Met Ile Gly Leu Phe Leu			
430	435	440		
tgg aag ttc tat cag tac aaa cag aaa agt	gca ttt caa gtc atg ggt			1516
Trp Lys Phe Tyr Gln Tyr Lys Gln Lys Ser	Ala Phe Gln Val Met Gly			
445	450	455		
tat tgc ctt cta aca gct aag ggt	gct gct gag act ctc aag ttc aac			1564
Tyr Cys Leu Leu Thr Ala Lys Gly Ala Ala	Glu Thr Leu Lys Phe Asn			
460	465	470		
atg gct tta ata ttg ttg cca gta tgc agg	aac acc att aca ttc ctc			1612
Met Ala Leu Ile Leu Leu Pro Val Cys Arg	Asn Thr Ile Thr Phe Leu			
475	480	485		
agg tct act aaa ttg agc tgg ttt gta ccc	ttt gat gac aac ata aac			1660
Arg Ser Thr Lys Leu Ser Cys Phe Val Pro	Phe Asp Asp Asn Ile Asn			
490	495	500	505	

ttt cac aag act gtt gct gca gcc att gtc act ggt atc ata ctc cat	1708
Phe His Lys Thr Val Ala Ala Ala Ile Val Thr Gly Ile Ile Leu His	
510 515 520	
gcc ggt aat cac ctt gta tgt gat ttc cca aag ctt ata cat gca aat	1756
Ala Gly Asn His Leu Val Cys Asp Phe Pro Lys Leu Ile His Ala Asn	
525 530 535	
agt acg aat tat cag aaa tat ttg gtg aat gat ttt ggc cca agc cag	1804
Ser Thr Asn Tyr Gln Lys Tyr Leu Val Asn Asp Phe Gly Pro Ser Gln	
540 545 550	
cct cag tac ata gat ctt gtt aaa gga gtg gag ggt gtg act gga ata	1852
Pro Gln Tyr Ile Asp Leu Val Lys Gly Val Glu Gly Val Thr Gly Ile	
555 560 565	
gtt atg gta atc ctc atg gcc att gct ttc act ctt gca acg cga tgg	1900
Val Met Val Ile Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Arg Trp	
570 575 580 585	
ttt agg cgg agc ctc att aag tta ccc aaa cct ttt gat aga ctc act	1948
Phe Arg Arg Ser Leu Ile Lys Leu Pro Lys Pro Phe Asp Arg Leu Thr	
590 595 600	
ggt ttc aat gcg ttc tgg tac tcg cac cac ctt ctc atc att gtc tac	1996
Gly Phe Asn Ala Phe Trp Tyr Ser His His Leu Leu Ile Ile Val Tyr	
605 610 615	
atc gta ctg atc atc cat ggc aca ttc ctc tac ctt gtg cat aac tgg	2044
Ile Val Leu Ile Ile His Gly Thr Phe Leu Tyr Leu Val His Asn Trp	
620 625 630	
tac tcc aaa acg aca tgg atg tat ata gca gtt cct gta ctt ctt tac	2092
Tyr Ser Lys Thr Thr Trp Met Tyr Ile Ala Val Pro Val Leu Leu Tyr	
635 640 645	
gca ggg gaa aga act ctt aga ttc ttc cga tca ggc tta tac agt gtc	2140
Ala Gly Glu Arg Thr Leu Arg Phe Phe Arg Ser Gly Leu Tyr Ser Val	
650 655 660 665	
cgg ctt cta aaa gta gca ata tat cct gga aat gtc ctt act ctg caa	2188
Arg Leu Leu Lys Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln	
670 675 680	
atg tct aag cct ccg caa ttt cga tac aag agt gga cag tat atg ttt	2236
Met Ser Lys Pro Pro Gln Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe	
685 690 695	
gtc cag tgt cca gct gtt tct cca ttc gag tgg cat cca ttt tcc att	2284
Val Gln Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile	
700 705 710	
act tca gct cct ggg gat gac tac ttg agc att cat atc cga caa ctt	2332
Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu	
715 720 725	
ggt gac tgg act caa gaa ctc aag cga gtg ttt tcc gag gct tgc gag	2380
Gly Asp Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu	
730 735 740 745	
cag cca gag gct gga aag agt ggc ctg ctc aga gct gac gaa aac acc	2428
Gln Pro Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr	
750 755 760	
aaa aca agt ttg cca aag cta tta ata gat gga cct tat gga gct cca	2476
Lys Thr Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro	
765 770 775	
gca caa gat tac cgg aag tat gat gtc tta ctg ctt gtt ggt ctt ggc	2524
Ala Gln Asp Tyr Arg Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly	
780 785 790	
att gga gca act ccc ttt ata agt atc ctg aaa gac ttg ctc aaa aac	2572
Ile Gly Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Lys Asn	
795 800 805	
atc gtc gca atg gag gag caa gca gat tta gtc tcg gat ttc agt gga	2620
Ile Val Ala Met Glu Glu Gln Ala Asp Leu Val Ser Asp Phe Ser Gly	
810 815 820 825	
aac tcg gac atg agt gct gca aca agt gaa caa cca gct ctc aac aag	2668

Asn Ser Asp Met Ser Ala Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys			
830	835	840	
att tct cca aaa aag aga aag agt act cta aaa acc aca aat gca tat			2716
Ile Ser Pro Lys Lys Arg Lys Ser Thr Leu Lys Thr Thr Asn Ala Tyr			
845	850	855	
ttt tat tgg gtg acc cgg gag caa gga tca ttt gat tgg ttc aaa ggt			2764
Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly			
860	865	870	
gtt atg aat gaa gtg gct gaa ctt gat caa agg ggt gtc atc gag atg			2812
Val Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met			
875	880	885	
cat aac tac ttg acg agt gtt tat gag gaa ggg gat gca cgt tca gct			2860
His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala			
890	895	900	905
ctc att acc atg gtc cag gca ctt aac cat gct aag aat ggg gtt gat			2908
Leu Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp			
910	915	920	
att gta tca ggc acc agt gtg agg aca cat ttc gcc agg ccg aat tgg			2956
Ile Val Ser Gly Thr Ser Val Arg Thr His Phe Ala Arg Pro Asn Trp			
925	930	935	
agg aaa gta ttt tcc aag acc tta acc aag cat gca aat gca aga ata			3004
Arg Lys Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile			
940	945	950	
gga gtt ttc tac tgt ggt gca ccc ata tta gct aaa gaa ctc agc caa			3052
Gly Val Phe Tyr Cys Gly Ala Pro Ile Leu Ala Lys Glu Leu Ser Gln			
955	960	965	
ctc tgc aaa gag ttt aac caa aag ggc aca aca aag ttc gag ttt cac			3100
Leu Cys Lys Glu Phe Asn Gln Lys Gly Thr Thr Lys Phe Glu Phe His			
970	975	980	985
aaa gaa cat ttt tagaagggcc tggagtatga ttaatcttgc atcaacggta			3152
Lys Glu His Phe			
cacacatcta tcttcggta cttatgtat tattctactg aagagataac attagtaagg			3212
aataagtca agataaattg tacataataag ggaagaagac tatttcaaga gaaaatacat			3272
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<211> 989

<212> PRT

<213> Lycopersicon esculentum

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Gly Asn Ile Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Ile Leu			
35	40	45	
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala			
50	55	60	
Thr Val Ile Asn Ile Asp Gly Ser Asp Pro Ala Ser Gly Val Gly Ile			
65	70	75	80
Gly Gly Ala Ser Ile Glu Thr Pro Ala Ser Val Thr Ser Thr Ser Glu			
85	90	95	
Thr Arg Ser Pro Met Met Arg Arg Ser Thr Ser Asn Lys Phe Arg Gln			
100	105	110	
Phe Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Lys His Phe			
115	120	125	
Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly			
130	135	140	
His Ala Ser Arg Ala Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val			
145	150	155	160

Val Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu
 165 170 175
 Arg Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Lys
 180 185 190
 Ala Leu Arg Gly Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp
 195 200 205
 Asn Glu Val Glu Asn Asn Phe Ala Lys Leu Ala Lys Asp Gly Tyr Leu
 210 215 220
 Tyr Arg Ser Asp Phe Ala Gln Cys Ile Gly Gln Tyr Ser Arg Arg Arg
 225 230 235 240
 Ser Leu Gln Phe Asn Tyr Arg Leu Ile Thr Leu Ile Leu Ile Asn Tyr
 245 250 255
 Leu Val Lys Gly Met Lys Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe
 260 265 270
 Asp Ala Leu Ser Arg Arg Arg Leu Lys Val Asp Lys Ile Ser Gln
 275 280 285
 Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr Asp Gln Ser Phe Asp
 290 295 300
 Ser Arg Leu Gln Ile Phe Phe Asp Met Val Asp Lys Asn Glu Asp Gly
 305 310 315 320
 Arg Ile Gly Glu Glu Val Lys Glu Ile Ile Met Leu Ser Ala Ser
 325 330 335
 Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala
 340 345 350
 Leu Ile Met Glu Glu Leu Asp Pro Glu Arg Leu Gly Tyr Ile Glu Leu
 355 360 365
 Trp Gln Leu Glu Thr Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr
 370 375 380
 Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser Gln Asn Leu Gln
 385 390 395 400
 Gly Leu Arg Lys Arg Ser Pro Ile Arg Arg Met Ser Thr Lys Leu Val
 405 410 415
 Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp Val Leu Val Leu Trp
 420 425 430
 Ile Leu Ile Met Ile Gly Leu Phe Leu Trp Lys Phe Tyr Gln Tyr Lys
 435 440 445
 Gln Lys Ser Ala Phe Gln Val Met Gly Tyr Cys Leu Leu Thr Ala Lys
 450 455 460
 Gly Ala Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Leu Pro
 465 470 475 480
 Val Cys Arg Asn Thr Ile Thr Phe Leu Arg Ser Thr Lys Leu Ser Cys
 485 490 495
 Phe Val Pro Phe Asp Asp Asn Ile Asn Phe His Lys Thr Val Ala Ala
 500 505 510
 Ala Ile Val Thr Gly Ile Ile Leu His Ala Gly Asn His Leu Val Cys
 515 520 525
 Asp Phe Pro Lys Leu Ile His Ala Asn Ser Thr Asn Tyr Gln Lys Tyr
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 Leu Val Asn Asp Phe Gly Pro Ser Gln Pro Gln Tyr Ile Asp Leu Val
 545 550 555 560
 Lys Gly Val Glu Gly Val Thr Gly Ile Val Met Val Ile Leu Met Ala
 565 570 575
 Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser Leu Ile Lys
 580 585 590
 Leu Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr
 595 600 605
 Ser His His Leu Leu Ile Ile Val Tyr Ile Val Leu Ile Ile His Gly
 610 615 620
 Thr Phe Leu Tyr Leu Val His Asn Trp Tyr Ser Lys Thr Thr Trp Met
 625 630 635 640
 Tyr Ile Ala Val Pro Val Leu Leu Tyr Ala Gly Glu Arg Thr Leu Arg

645	650	655	
Phe Phe Arg Ser Gly Leu Tyr Ser Val Arg Leu Leu Lys Val Ala Ile			
660	665	670	
Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Pro Gln Phe			
675	680	685	
Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser			
690	695	700	
Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp			
705	710	715	720
Tyr Leu Ser Ile His Ile Arg Gln Leu Gly Asp Trp Thr Gln Glu Leu			
725	730	735	
Lys Arg Val Phe Ser Glu Ala Cys Glu Gln Pro Glu Ala Gly Lys Ser			
740	745	750	
Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys Thr Ser Leu Pro Lys Leu			
755	760	765	
Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr			
770	775	780	
Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile			
785	790	795	800
Ser Ile Leu Lys Asp Leu Leu Lys Asn Ile Val Ala Met Glu Glu Gln			
805	810	815	
Ala Asp Leu Val Ser Asp Phe Ser Gly Asn Ser Asp Met Ser Ala Ala			
820	825	830	
Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser Pro Lys Lys Arg Lys			
835	840	845	
Ser Thr Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr Arg Glu			
850	855	860	
Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Val Ala Glu			
865	870	875	880
Leu Asp Gln Arg Gly Val Ile Glu Met His Asn Tyr Leu Thr Ser Val			
885	890	895	
Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Val Gln Ala			
900	905	910	
Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Ser Val			
915	920	925	
Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Phe Ser Lys Thr			
930	935	940	
Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val Phe Tyr Cys Gly Ala			
945	950	955	960
Pro Ile Leu Ala Lys Glu Leu Ser Gln Leu Cys Lys Glu Phe Asn Gln			
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Lys Gly Thr Thr Lys Phe Glu Phe His Lys Glu His Phe			
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Ser Phe Asp Ser Val Ser Ala Gly Lys Thr Ala Val Gly Ser Ala Ser
15 20 25

act tca ccg gga act gaa tac tcc att aac ggt gat caa gag ttc gtt	146
Thr Ser Pro Gly Thr Glu Tyr Ser Ile Asn Gly Asp Gln Glu Phe Val	
30 35 40	
gaa gtc aca atc gat ctt caa gac gat gac aca atc gtt ctt cgt agc	194
Glu Val Thr Ile Asp Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser	
45 50 55 60	
gtc gag cca gca acc gcc att aat gtc atc gga gat atc tcc gac gac	242
Val Glu Pro Ala Thr Ala Ile Asn Val Ile Gly Asp Ile Ser Asp Asp	
65 70 75	
aac acc gga ata atg act ccg gtt tcg att tcg aga tct ccg acg atg	290
Asn Thr Gly Ile Met Thr Pro Val Ser Ile Ser Arg Ser Pro Thr Met	
80 85 90	
aaa cga act tca tct aat cgg ttc cga caa ttc tca caa gag ctt aaa	338
Lys Arg Thr Ser Ser Asn Arg Phe Arg Gln Phe Ser Gln Glu Leu Lys	
95 100 105	
gcc gaa gct gtg gcg aaa gcg aaa cag tta tct cag gag ttg aaa cga	386
Ala Glu Ala Val Ala Lys Ala Lys Gln Leu Ser Gln Glu Leu Lys Arg	
110 115 120	
ttc tca tgg tct cgt tct ttc tca ggt aac tta acc act act agt acc	434
Phe Ser Trp Ser Arg Ser Phe Ser Gly Asn Leu Thr Thr Thr Ser Thr	
125 130 135 140	
gcc gct aat caa agc ggc ggt gct ggt ggt ttg gtg aac tcg gct	482
Ala Ala Asn Gln Ser Gly Gly Ala Gly Gly Leu Val Asn Ser Ala	
145 150 155	
tta gaa gcg cga gcg ttg cga aag caa cgt gct cag tta gat cgg act	530
Leu Glu Ala Arg Ala Leu Arg Lys Gln Arg Ala Gln Leu Asp Arg Thr	
160 165 170	
cggtctagt gct caa aga gct ctt cgt ggt ttg aga ttc att agc aat	578
Arg Ser Ser Ala Gln Arg Ala Leu Arg Gly Leu Arg Phe Ile Ser Asn	
175 180 185	
aag caa aag aac gtt gat ggt tgg aac gat gtt caa tca aat ttc gaa	626
Lys Gln Lys Asn Val Asp Gly Trp Asn Asp Val Gln Ser Asn Phe Glu	
190 195 200	
aaa ttc gaa aaa aat ggt tac atc tat cgc tcc gat ttc gct caa tgc	674
Lys Phe Glu Lys Asn Gly Tyr Ile Tyr Arg Ser Asp Phe Ala Gln Cys	
205 210 215 220	
ata gga atg aaa gat tcg aaa gaa ttt gca ttg gaa ctg ttc gat gca	722
Ile Gly Met Lys Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe Asp Ala	
225 230 235	
ttg agt aga aga aga tta aaa gta gag aaa atc aat cac gat gag	770
Leu Ser Arg Arg Arg Leu Lys Val Glu Lys Ile Asn His Asp Glu	
240 245 250	
ctt tat gag tat tgg tca caa atc aac gac gag agt ttt gat tct cgt	818
Leu Tyr Glu Tyr Trp Ser Gln Ile Asn Asp Glu Ser Phe Asp Ser Arg	
255 260 265	
ctc cag atc ttc ttc gac ata gtg gac aag aat gaa gat ggg aga att	866
Leu Gln Ile Phe Phe Asp Ile Val Asp Lys Asn Glu Asp Gly Arg Ile	
270 275 280	
aca gaa gag gaa gta aaa gag ata ata atg ttg agt gca tct gca aat	914
Thr Glu Glu Glu Val Lys Glu Ile Ile Met Leu Ser Ala Ser Ala Asn	
285 290 295 300	
aag cta tca aga tta aag gaa caa gca gag gaa tat gca gct ttg att	962
Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala Leu Ile	
305 310 315	
atg gaa gag tta gat cct gaa aga ctt ggc tac ata gag cta tgg caa	1010
Met Glu Glu Leu Asp Pro Glu Arg Leu Gly Tyr Ile Glu Leu Trp Gln	
320 325 330	
cta gag act ttg ctt cta caa aaa gac aca tac ctc aat tac agt caa	1058
Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr Ser Gln	
335 340 345	
gca ttg agc tat acg agc caa gca ttg agc caa aac ctt caa ggg tta	1106

Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	Gln	Asn	Leu	Gln	Gly	Leu	
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agg	gga	aag	agt	cga	ata	cat	aga	atg	agt	tcg	gat	ttc	gtc	tac	att	1154
Arg	Gly	Lys	Ser	Arg	Ile	His	Arg	Met	Ser	Ser	Asp	Phe	Val	Tyr	Ile	
365					370				375					380		
atg	caa	gag	aat	tgg	aaa	agg	ata	tgg	gtt	tta	tcc	tta	tgg	atc	atg	1202
Met	Gln	Glu	Asn	Trp	Lys	Arg	Ile	Trp	Val	Leu	Ser	Leu	Trp	Ile	Met	
					385				390				395			
atc	atg	atc	gga	tta	ttc	ttg	tgg	aaa	ttc	ttc	caa	tac	aag	caa	aaa	1250
Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp	Lys	Phe	Phe	Gln	Tyr	Lys	Gln	Lys	
					400				405				410			
gat	gca	ttt	cat	gtg	atg	gga	tat	tgt	tta	ctc	aca	gcc	aaa	gga	gca	1298
Asp	Ala	Phe	His	Val	Met	Gly	Tyr	Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	
					415			420				425				
gct	gaa	aca	ctt	aaa	ttc	aac	atg	gct	cta	ata	ctt	ttc	cca	gtt	tgc	1346
Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	Phe	Pro	Val	Cys	
					430			435			440					
aga	aac	acc	att	act	tgg	ctt	aga	tcc	aca	aga	ctc	tct	tac	ttc	gtt	1394
Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr	Arg	Leu	Ser	Tyr	Phe	Val	
					445			450			455			460		
cct	ttt	gat	gat	aat	atc	aac	ttc	cac	aag	aca	att	gct	gga	gcc	att	1442
Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	Thr	Ile	Ala	Gly	Ala	Ile	
					465			470			475					
gta	gta	gct	gtg	atc	ctt	cat	att	gga	gac	cat	ctt	gct	tgt	gat	ttc	1490
Val	Val	Ala	Val	Ile	Leu	His	Ile	Gly	Asp	His	Leu	Ala	Cys	Asp	Phe	
					480			485			490					
cct	aga	att	gtt	aga	gcc	acc	gaa	tac	gat	tac	aat	cgg	tat	ctg	ttt	1538
Pro	Arg	Ile	Val	Arg	Ala	Thr	Glu	Tyr	Asp	Tyr	Asn	Arg	Tyr	Leu	Phe	
					495			500			505					
cat	tac	ttt	caa	aca	aaa	cag	cca	aca	tac	ttc	gac	ctc	gtt	aag	gga	1586
His	Tyr	Phe	Gln	Thr	Lys	Gln	Pro	Thr	Tyr	Phe	Asp	Leu	Val	Lys	Gly	
					510			515			520					
cct	gaa	gga	atc	act	ggg	att	tta	atg	gtc	att	ttg	atg	att	att	tca	1634
Pro	Glu	Gly	Ile	Thr	Gly	Ile	Leu	Met	Val	Ile	Leu	Met	Ile	Ile	Ser	
					525			530			535			540		
ttc	aca	tta	gca	aca	aga	tgg	ttt	agg	cgt	aac	cta	gtc	aag	ctt	cct	1682
Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Asn	Leu	Val	Lys	Leu	Pro	
					545			550			555			555		
aag	cca	ttt	gat	cga	cta	acc	ggt	ttt	aac	gcc	ttt	tgg	tat	tcg	cat	1730
Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	
					560			565			570					
cat	ttg	ttc	gtc	att	gtt	tat	atc	ttg	ctt	att	ctt	cat	gg	atc	ttc	1778
His	Leu	Phe	Val	Ile	Val	Tyr	Ile	Leu	Leu	Ile	Leu	His	Gly	Ile	Phe	
					575			580			585					
ctc	tat	ttc	gcc	aag	cct	tgg	tat	gtt	cgt	acg	aca	tgg	atg	tat	ctt	1826
Leu	Tyr	Phe	Ala	Lys	Pro	Trp	Tyr	Val	Arg	Thr	Thr	Trp	Met	Tyr	Leu	
					590			595			600					
gca	gta	cca	gtt	tta	ctc	tat	ggt	gga	gaa	aga	aca	ctt	agg	tac	ttc	1874
Ala	Val	Pro	Val	Leu	Leu	Tyr	Gly	Gly	Glu	Arg	Thr	Leu	Arg	Tyr	Phe	
					605			610			615			620		
cgt	tct	ggt	tct	tat	tcg	gtt	cga	ctg	ctt	aag	gtt	gct	ata	tat	cct	1922
Arg	Ser	Gly	Ser	Tyr	Ser	Val	Arg	Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	
					625			630			635					
ggt	aat	gtt	cta	acg	cta	caa	atg	tcg	aaa	cca	act	caa	ttt	cgt	tac	1970
Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	Lys	Pro	Thr	Gln	Phe	Arg	Tyr	
					640			645			650					
aaa	agc	gga	caa	tac	atg	ttt	gtc	caa	tgt	cct	gcg	gtt	tcg	cca	ttc	2018
Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	
					655			660			665					
gag	tgg	cat	cca	ttc	tca	att	act	tcc	gca	cct	gaa	gat	gat	tat	atc	2066
Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Glu	Asp	Asp	Tyr	Ile	

670	675	680	
agc att cac att aga caa ctt ggt gat tgg act caa gaa ctc aaa aga			2114
Ser Ile His Ile Arg Gln Leu Gly Asp Trp Thr Gln Glu Leu Lys Arg			
685	690	695	700
gta ttc tct gaa gtt tgt gag cca ccg gtt ggc ggt aaa agc gga ctt			2162
Val Phe Ser Glu Val Cys Glu Pro Pro Val Gly Gly Lys Ser Gly Leu			
705	710	715	
ctc aga gcc gac gaa aca aca aag aaa agt ttg cca aag cta ttg ata			2210
Leu Arg Ala Asp Glu Thr Thr Lys Lys Ser Leu Pro Lys Leu Leu Ile			
720	725	730	
gat gga ccg tac ggt gca cca gca caa gat tat agg aaa tat gat gtt			2258
Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr Asp Val			
735	740	745	
ctc tta tta gtt ggt ctt ggc att ggt gca act cca ttt atc agt atc			2306
Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile Ser Ile			
750	755	760	
ttg aaa gat ttg ctt aac aac att gtt aaa atg gaa gag cat gcg gat			2354
Leu Lys Asp Leu Leu Asn Asn Ile Val Lys Met Glu Glu His Ala Asp			
765	770	775	780
tcg atc tcg gat ttc agt aga tca tca gaa tac agc aca gga agc aac			2402
Ser Ile Ser Asp Phe Ser Arg Ser Ser Glu Tyr Ser Thr Gly Ser Asn			
785	790	795	
ggt gac acg cca aga cga aag aga ata cta aaa acc aca aat gct tat			2450
Gly Asp Thr Pro Arg Arg Lys Arg Ile Leu Lys Thr Thr Asn Ala Tyr			
800	805	810	
ttc tac tgg gtc aca aga gaa caa ggc tct ttt gat tgg ttc aaa ggt			2498
Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly			
815	820	825	
gtc atg aac gaa gtt gca gaa ctt gac caa ccg ggt gtg ata gag atg			2546
Val Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met			
830	835	840	
cat aac tat tta aca agt gtg tat gaa gaa ggt gat gct cgt tct gct			2594
His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala			
845	850	855	860
ctc att aca atg gtt caa gct ctt aat cat gcc aaa aat ggt gtc gac			2642
Leu Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp			
865	870	875	
att gtc tct ggc act agg gtc aga aca cac ttt gca aga cct aat tgg			2690
Ile Val Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp			
880	885	890	
aag aag gtt ctc aca aag cta agt tcc aag cat tgc aat gca aga aca			2738
Lys Lys Val Leu Thr Lys Leu Ser Ser Lys His Cys Asn Ala Arg Thr			
895	900	905	
gga gtg ttt tat tgc gga gta ccg gtt tta ggg aag gag ctt agc aaa			2786
Gly Val Phe Tyr Cys Gly Val Pro Val Leu Gly Lys Glu Leu Ser Lys			
910	915	920	
cta tgc aac aca ttc aat caa aaa ggt tca acc aag ttt gaa ttt cac			2834
Leu Cys Asn Thr Phe Asn Gln Lys Gly Ser Thr Lys Phe Glu Phe His			
925	930	935	940
aag gag cat ttc taaaagacaa gaaggaagaa gccaaaagcc ctcttagattc			2886
Lys Glu His Phe			
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aagtgattaa acgttaaacac actgtcaaaa gtgagtgtgt taacgtttag ctccacacgt			3006
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<213> Arabidopsis thaliana

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 Asp Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala
 50 55 60
 Thr Ala Ile Asn Val Ile Gly Asp Ile Ser Asp Asp Asn Thr Gly Ile
 65 70 75 80
 Met Thr Pro Val Ser Ile Ser Arg Ser Pro Thr Met Lys Arg Thr Ser
 85 90 95
 Ser Asn Arg Phe Arg Gln Phe Ser Gln Glu Leu Lys Ala Glu Ala Val
 100 105 110
 Ala Lys Ala Lys Gln Leu Ser Gln Glu Leu Lys Arg Phe Ser Trp Ser
 115 120 125
 Arg Ser Phe Ser Gly Asn Leu Thr Thr Ser Thr Ala Ala Asn Gln
 130 135 140
 Ser Gly Gly Ala Gly Gly Leu Val Asn Ser Ala Leu Glu Ala Arg
 145 150 155 160
 Ala Leu Arg Lys Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala
 165 170 175
 Gln Arg Ala Leu Arg Gly Leu Arg Phe Ile Ser Asn Lys Gln Lys Asn
 180 185 190
 Val Asp Gly Trp Asn Asp Val Gln Ser Asn Phe Glu Lys Phe Glu Lys
 195 200 205
 Asn Gly Tyr Ile Tyr Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys
 210 215 220
 Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg
 225 230 235 240
 Arg Arg Leu Lys Val Glu Lys Ile Asn His Asp Glu Leu Tyr Glu Tyr
 245 250 255
 Trp Ser Gln Ile Asn Asp Glu Ser Phe Asp Ser Arg Leu Gln Ile Phe
 260 265 270
 Phe Asp Ile Val Asp Lys Asn Glu Asp Gly Arg Ile Thr Glu Glu Glu
 275 280 285
 Val Lys Glu Ile Ile Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg
 290 295 300
 Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu
 305 310 315 320
 Asp Pro Glu Arg Leu Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu
 325 330 335
 Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr
 340 345 350
 Thr Ser Gln Ala Leu Ser Gln Asn Leu Gln Gly Leu Arg Gly Lys Ser
 355 360 365
 Arg Ile His Arg Met Ser Ser Asp Phe Val Tyr Ile Met Gln Glu Asn
 370 375 380
 Trp Lys Arg Ile Trp Val Leu Ser Leu Trp Ile Met Ile Met Ile Gly
 385 390 395 400
 Leu Phe Leu Trp Lys Phe Phe Gln Tyr Lys Gln Lys Asp Ala Phe His
 405 410 415
 Val Met Gly Tyr Cys Leu Leu Thr Ala Lys Gly Ala Ala Glu Thr Leu
 420 425 430
 Lys Phe Asn Met Ala Leu Ile Leu Phe Pro Val Cys Arg Asn Thr Ile
 435 440 445
 Thr Trp Leu Arg Ser Thr Arg Leu Ser Tyr Phe Val Pro Phe Asp Asp
 450 455 460
 Asn Ile Asn Phe His Lys Thr Ile Ala Gly Ala Ile Val Val Ala Val
 465 470 475 480

Ile Leu His Ile Gly Asp His Leu Ala Cys Asp Phe Pro Arg Ile Val
 485 490 495
 Arg Ala Thr Glu Tyr Asp Tyr Asn Arg Tyr Leu Phe His Tyr Phe Gln
 500 505 510
 Thr Lys Gln Pro Thr Tyr Phe Asp Leu Val Lys Gly Pro Glu Gly Ile
 515 520 525
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 Ser Lys Lys Asn Ala Arg Phe Ala Asp Asp Leu Pro Lys Arg Ser Asn
 50 55 60
 Ser Val Ala Gly Gly Arg Gly Asp Asp Glu Tyr Val Glu Ile Thr
 65 70 75 80
 Leu Asp Ile Arg Asp Asp Ser Val Ala Val His Ser Val Gln Gln Ala
 85 90 95
 Ala Gly Gly Gly His Leu Glu Asp Pro Glu Leu Ala Leu Leu Thr
 100 105 110
 Lys Lys Thr Leu Glu Ser Ser Leu Asn Asn Thr Thr Ser Leu Ser Phe
 115 120 125
 Phe Arg Ser Thr Ser Ser Arg Ile Lys Asn Ala Ser Arg Glu Leu Arg
 130 135 140
 Arg Val Phe Ser Arg Arg Pro Ser Pro Ala Val Arg Arg Phe Asp Arg
 145 150 155 160
 Thr Ser Ser Ala Ala Ile His Ala Leu Lys Gly Leu Lys Phe Ile Ala
 165 170 175
 Thr Lys Thr Ala Ala Trp Pro Ala Val Asp Gln Arg Phe Asp Lys Leu
 180 185 190
 Ser Ala Asp Ser Asn Gly Leu Leu Ser Ala Lys Phe Trp Glu Cys
 195 200 205
 Leu Gly Met Asn Lys Glu Ser Lys Asp Phe Ala Asp Gln Leu Phe Arg
 210 215 220
 Ala Leu Ala Arg Arg Asn Asn Val Ser Gly Asp Ala Ile Thr Lys Glu
 225 230 235 240
 Gln Leu Arg Ile Phe Trp Glu Gln Ile Ser Asp Glu Ser Phe Asp Ala
 245 250 255
 Lys Leu Gln Val Phe Phe Asp Met Val Asp Lys Asp Glu Asp Gly Arg
 260 265 270
 Val Thr Glu Glu Glu Val Ala Glu Ile Ile Ser Leu Ser Ala Ser Ala
 275 280 285
 Asn Lys Leu Ser Asn Ile Gln Lys Gln Ala Lys Glu Tyr Ala Ala Leu
 290 295 300
 Ile Met Glu Glu Leu Asp Pro Asp Asn Ala Gly Phe Ile Met Ile Glu
 305 310 315 320
 Asn Leu Glu Met Leu Leu Gln Ala Pro Asn Gln Ser Val Arg Met
 325 330 335
 Gly Asp Ser Arg Ile Leu Ser Gln Met Leu Ser Gln Lys Leu Arg Pro
 340 345 350
 Ala Lys Glu Ser Asn Pro Leu Leu Arg Trp Ser Glu Lys Ile Lys Tyr
 355 360 365
 Phe Ile Leu Asp Asn Trp Gln Arg Leu Trp Ile Met Met Leu Trp Leu
 370 375 380
 Gly Ile Cys Gly Gly Leu Phe Thr Tyr Lys Phe Ile Gln Tyr Lys Asn

385	390	395	400
Lys Ala Ala Tyr Gly Val Met Gly Tyr Cys Val Cys Val Ala Lys Gly			
405	410	415	
Gly Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Leu Pro Val			
420	425	430	
Cys Arg Asn Thr Ile Thr Trp Leu Arg Asn Lys Thr Lys Leu Gly Thr			
435	440	445	
Val Val Pro Phe Asp Asp Ser Leu Asn Phe His Lys Val Ile Ala Ser			
450	455	460	
Gly Ile Val Val Gly Val Leu Leu His Ala Gly Ala His Leu Thr Cys			
465	470	475	480
Asp Phe Pro Arg Leu Ile Ala Ala Asp Glu Asp Thr Tyr Glu Pro Met			
485	490	495	
Glu Lys Tyr Phe Gly Asp Gln Pro Thr Ser Tyr Trp Trp Phe Val Lys			
500	505	510	
Gly Val Glu Gly Trp Thr Gly Ile Val Met Val Val Leu Met Ala Ile			
515	520	525	
Ala Phe Thr Leu Ala Thr Pro Trp Phe Arg Arg Asn Lys Leu Asn Leu			
530	535	540	
Pro Asn Phe Leu Lys Lys Leu Thr Gly Phe Asn Ala Phe Trp Tyr Thr			
545	550	555	560
His His Leu Phe Ile Ile Val Tyr Ala Leu Leu Ile Val His Gly Ile			
565	570	575	
Lys Leu Tyr Leu Thr Lys Ile Trp Tyr Gln Lys Thr Thr Trp Met Tyr			
580	585	590	
Leu Ala Val Pro Ile Leu Leu Tyr Ala Ser Glu Arg Leu Leu Arg Ala			
595	600	605	
Phe Arg Ser Ser Ile Lys Pro Val Lys Met Ile Lys Val Ala Val Tyr			
610	615	620	
Pro Gly Asn Val Leu Ser Leu His Met Thr Lys Pro Gln Gly Phe Lys			
625	630	635	640
Tyr Lys Ser Gly Gln Phe Met Leu Val Asn Cys Arg Ala Val Ser Pro			
645	650	655	
Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr			
660	665	670	
Leu Ser Val His Ile Arg Thr Leu Gly Asp Trp Thr Arg Lys Leu Arg			
675	680	685	
Thr Val Phe Ser Glu Val Cys Lys Pro Pro Thr Ala Gly Lys Ser Gly			
690	695	700	
Leu Leu Arg Ala Asp Gly Gly Asp Gly Asn Leu Pro Phe Pro Lys Val			
705	710	715	720
Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr			
725	730	735	
Asp Val Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile			
740	745	750	
Ser Ile Leu Lys Asp Ile Ile Asn Asn Met Lys Gly Pro Asp Arg Asp			
755	760	765	
Ser Asp Ile Glu Asn Asn Asn Ser Asn Asn Asn Ser Lys Gly Phe Lys			
770	775	780	
Thr Arg Lys Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe			
785	790	795	800
Glu Trp Phe Lys Gly Ile Met Asp Glu Ile Ser Glu Leu Asp Glu Glu			
805	810	815	
Gly Ile Ile Glu Leu His Asn Tyr Cys Thr Ser Val Tyr Glu Glu Gly			
820	825	830	
Asp Ala Arg Val Ala Leu Ile Ala Met Leu Gln Ser Leu Gln His Ala			
835	840	845	
Lys Asn Gly Val Asp Val Val Ser Gly Thr Arg Val Lys Ser His Phe			
850	855	860	
Ala Lys Pro Asn Trp Arg Gln Val Tyr Lys Lys Ile Ala Val Gln His			
865	870	875	880

Pro Gly Lys Arg Ile Gly Val Phe Tyr Cys Gly Met Pro Gly Met Ile
 885 890 895
 Lys Glu Leu Lys Asn Leu Ala Leu Asp Phe Ser Arg Lys Thr Thr Thr
 900 905 910
 Lys Phe Asp Phe His Lys Glu Asn Phe
 915 920

<210> 15
 <211> 3338
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> CDS
 <222> (313)..(3129)
 <223> coding for NADPH oxidase

<220>
 <221> misc_feature
 <222> (1952)..(1952)
 <223> n is a, c, g, or t

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 gaaaagaaaga cagaaaagact cggctttctt tcttctcttg gtctgaaact cccaaataga 120
 ataccaatta ttaatctttt gtcattttt tccttctcgc gttcatatat actggaatat 180
 acatcttttt ttcaacctat cttctttcat tttcaagaat tcgggttcca taaatagtag 240
 gttcaactact ttatattcaa ctcctttaaa gtttattcat tcattttt tctcaaagaa 300
 aaaactatag aa atg caa aat tcg gaa aat cat cat ccg cac cac cag cac 351
 Met Gln Asn Ser Glu Asn His His Pro His His Gln His
 1 5 10
 cac cat tcg gac aca gag ata att gga aat gat aga gcg tcg tac agt 399
 His His Ser Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser
 15 20 25
 ggt ccg tta agc gga ccg tta aac aaa cga ggc ggc aaa aag agt gcg 447
 Gly Pro Leu Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Ser Ala
 30 35 40 45
 aga ttt aac att cct gaa tct acc gac atc gga acc agt gtc gga acc 495
 Arg Phe Asn Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr
 50 55 60
 ggc ggc aag tcc aat gat gat gcg tac gtt gaa atc act ctc gat gtc 543
 Gly Gly Lys Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val
 65 70 75
 cgc gaa gat tcc gtc gct gtc cac agt gtc aaa act gcc ggc ggt gat 591
 Arg Glu Asp Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp
 80 85 90
 gac gtg gaa gat ccc gag ctg gct tta ttg gct aaa ggc tta gag aag 639
 Asp Val Glu Asp Pro Glu Leu Ala Leu Ala Lys Gly Leu Glu Lys
 95 100 105
 aag tcc act tta gga tct tca ctt gtt cga aat gct tcg tct aga att 687
 Lys Ser Thr Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile
 110 115 120 125
 cgg caa gtg tca caa gag ctc agg cgt ttg gct tcc tta aat aaa cgc 735
 Arg Gln Val Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg
 130 135 140
 cca att cct act gga agg ttc gac agg aat aaa tca gct gct gct cat 783
 Pro Ile Pro Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His
 145 150 155
 gct ctt aaa ggt ctc aag ttt att agt aag acc gac ggc ggc gct ggt 831
 Ala Leu Lys Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly
 160 165 170

tgg	gcc	gcc	gtc	gag	aag	cg	ttc	gat	gag	att	act	gct	tct	act	act	879	
Trp	Ala	Ala	Val	Glu	Lys	Arg	Phe	Asp	Glu	Ile	Thr	Ala	Ser	Thr	Thr		
175				180						185							
ggt	ttg	c	c	cgt	gcc	aaa	ttt	gga	gaa	tgt	ata	ggt	atg	aat	aag	927	
Gly	Leu	Leu	Pro	Arg	Ala	Lys	Phe	Gly	Glu	Cys	Ile	Gly	Met	Asn	Lys		
190				195				200			205						
gag	tct	a	a	gaa	ttt	g	c	ttt	g	g	at	g	c	gg	agg	975	
Glu	Ser	Lys	Glu	Phe	Ala	Val	Glu	Leu	Tyr	Asp	Ala	Leu	Ala	Arg	Arg		
				210				215			220						
aga	aa	att	aca	act	gat	tcc	att	aa	ca	cag	ctc	aa	gag	ttc		1023	
Arg	Asn	Ile	Thr	Asp	Ser	Ile	Asn	Lys	Ala	Gln	Leu	Lys	Glu	Phe			
				225				230			235						
tgg	gac	caa	gtg	gct	gac	caa	agt	ttt	gat	tct	cgc	ctt	caa	aca	ttt	1071	
Trp	Asp	Gln	Val	Ala	Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Thr	Phe		
				240				245			250						
ttt	gac	atg	gtt	gat	aaa	gat	gct	gat	ggt	aga	att	aca	gaa	gaa	gaa	1119	
Phe	Asp	Met	Val	Asp	Lys	Asp	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Glu	Glu		
				255				260			265						
gtc	aga	gag	att	ata	ggc	ctt	agc	g	cg	tcg	gcc	aa	agg	ctg	tca	aca	1167
Val	Arg	Glu	Ile	Ile	Gly	Leu	Ser	Ala	Ser	Ala	Asn	Arg	Leu	Ser	Thr		
				270				275			280			285			
atc	cag	aaa	caa	gct	gat	gaa	tac	gca	gca	atg	atc	atg	gaa	gag	ttg	1215	
Ile	Gln	Lys	Gln	Ala	Asp	Glu	Tyr	Ala	Ala	Met	Ile	Met	Glu	Glu	Leu		
				290				295			300						
gat	cct	aa	ac	ctc	gga	tac	att	atg	att	gag	aa	ttg	gaa	atg	ctt	1263	
Asp	Pro	Asn	Asn	Leu	Gly	Tyr	Ile	Met	Ile	Glu	Asn	Leu	Glu	Met	Leu		
				305				310			315						
tta	ctg	caa	gca	cca	aat	caa	tca	gtg	caa	aga	gga	ggc	gaa	agt	cg	1311	
Leu	Leu	Gln	Ala	Pro	Asn	Gln	Ser	Val	Gln	Arg	Gly	Gly	Glu	Ser	Arg		
				320				325			330						
aac	ttg	agt	caa	atg	cta	agt	caa	aaa	cta	aag	cat	aca	caa	gag	aga	1359	
Asn	Leu	Ser	Gln	Met	Leu	Ser	Gln	Lys	Leu	Lys	His	Thr	Gln	Glu	Arg		
				335				340			345						
aat	cca	ata	gta	aga	tgg	tac	aag	agt	ttc	atg	tac	ttt	ttg	ctg	gat	1407	
Asn	Pro	Ile	Val	Arg	Trp	Tyr	Lys	Ser	Phe	Met	Tyr	Phe	Leu	Leu	Asp		
				350				355			360			365			
aat	tgg	caa	aga	gtt	tgg	gta	ttt	tta	ctg	tgg	att	gga	att	atg	gct	1455	
Asn	Trp	Gln	Arg	Val	Trp	Val	Leu	Leu	Leu	Trp	Ile	Gly	Ile	Met	Ala		
				370				375			380						
ggt	cta	ttt	aca	tgg	aaa	tat	ata	cag	tat	aaa	gaa	aaa	gct	gca	tat	1503	
Gly	Leu	Phe	Thr	Trp	Lys	Tyr	Ile	Gln	Tyr	Lys	Glu	Lys	Ala	Ala	Tyr		
				385				390			395						
aaa	gtc	atg	gg	ccc	tgt	gtg	tgt	ttt	gcc	aa	gg	aa	gg	ct	gca	ata	1551
Lys	Val	Met	Gly	Pro	Cys	Val	Cys	Phe	Ala	Lys	Gly	Ala	Ala	Glu	Thr		
				400				405			410						
ctc	aag	ctc	aa	atg	gca	att	att	tta	ttt	ccg	gtt	tgc	aga	aa	ac	1599	
Leu	Lys	Leu	Asn	Met	Ala	Ile	Ile	Leu	Phe	Pro	Val	Cys	Arg	Asn	Thr		
				415				420			425						
atc	aca	tgg	ctt	cga	aat	aag	acc	aga	tta	ggt	gct	gct	gtt	cct	ttt	1647	
Ile	Thr	Trp	Leu	Arg	Asn	Lys	Thr	Arg	Leu	Gly	Ala	Ala	Val	Pro	Phe		
				430				435			440			445			
gat	gat	aa	cc	ttt	cac	aa	gtg	ata	gca	gtg	gca	att	gct	ctt		1695	
Asp	Asp	Asn	Leu	Asn	Phe	His	Lys	Val	Ile	Ala	Val	Ala	Ile	Ala	Leu		
				450				455			460						
ggg	gtt	gga	ata	cac	gga	ctt	cac	ttt	aca	tgt	gat	ttt	cct	cg		1743	
Gly	Val	Gly	Ile	His	Gly	Leu	Ser	His	Leu	Thr	Cys	Asp	Phe	Pro	Arg		
				465				470			475						
ctt	tta	aat	gct	agt	g	aa	g	aa	ttt	g	aa	t	ac	t	ttt	1791	
Leu	Leu	Asn	Ala	Ser	Glu	Glu	Tyr	Glu	Pro	Met	Lys	Tyr	Tyr	Phe			
				480				485			490						
gga	gat	c	g	aa	g	ac	t	ttt	g	ttt	ata	aa	g	g	gg	1839	

Gly	Asp	Gln	Pro	Glu	Ser	Tyr	Trp	Trp	Phe	Ile	Lys	Gly	Val	Glu	Gly	
495				500					505							
gta	act	gga	att	ata	atg	gtg	gtt	tta	atg	gca	ata	gca	ttt	act	cta	1887
Val	Thr	Gly	Ile	Ile	Met	Val	Val	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	
510				515					520				525			
gca	acc	cca	tgg	ttt	aga	agg	aat	aga	gtt	agt	ttg	cca	aaa	cca	ttt	1935
Ala	Thr	Pro	Trp	Phe	Arg	Arg	Asn	Arg	Val	Ser	Leu	Pro	Lys	Pro	Phe	
				530					535				540			
cac	aaa	ctc	act	gga	tnt	aat	gcc	ttt	tgg	tac	tct	cac	cat	ctc	ttt	1983
His	Lys	Leu	Thr	Gly	Xaa	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Phe	
				545				550				555				
gtt	atc	gtc	tac	act	ctg	ttc	att	gtg	cat	ggt	gaa	aag	cta	tac	att	2031
Val	Ile	Val	Tyr	Thr	Leu	Phe	Ile	Val	His	Gly	Glu	Lys	Leu	Tyr	Ile	
				560				565				570				
acc	aaa	gat	tgg	tac	aag	aga	acc	gac	atg	gat	gta	ctt	tta	act	atc	2079
Thr	Lys	Asp	Trp	Tyr	Lys	Arg	Thr	Asp	Met	Asp	Val	Leu	Leu	Thr	Ile	
				575				580				585				
cca	atc	ata	ctc	tat	gct	agt	gaa	agg	ttg	att	agg	gca	ttc	agg	tca	2127
Pro	Ile	Ile	Leu	Tyr	Ala	Ser	Glu	Arg	Leu	Ile	Arg	Ala	Phe	Arg	Ser	
				590				595				600		605		
agc	att	aaa	gct	gtt	aag	att	ttg	aag	gtg	gca	gta	tat	cca	gga	aat	2175
Ser	Ile	Lys	Ala	Val	Lys	Ile	Leu	Lys	Val	Ala	Val	Tyr	Pro	Gly	Asn	
				610				615				620				
gtg	ttg	gca	ctt	cac	atg	tca	aaa	cca	cag	ggc	tac	aaa	tac	aaa	agt	2223
Val	Leu	Ala	Leu	His	Met	Ser	Lys	Pro	Gln	Gly	Tyr	Lys	Tyr	Lys	Ser	
				625				630				635				
ggg	caa	tac	atg	ttt	gtc	aac	tgt	gct	gca	gtt	tct	cca	ttt	gag	tgg	2271
Gly	Gln	Tyr	Met	Phe	Val	Asn	Cys	Ala	Ala	Val	Ser	Pro	Phe	Glu	Trp	
				640				645				650				
cat	cca	ttt	tca	att	act	tcg	gcc	cca	gga	gat	gac	tat	ctc	agt	gtc	2319
His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Val	
				655				660				665				
cat	att	cga	act	ctt	ggt	gat	tgg	acc	agg	caa	ctt	aaa	act	gtt	ttc	2367
His	Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Arg	Gln	Leu	Lys	Thr	Val	Phe	
				670				675				680		685		
tcc	gag	gtt	tgc	cag	cca	cca	cct	aat	gga	aaa	agt	gga	ctc	ctc	aga	2415
Ser	Glu	Val	Cys	Gln	Pro	Pro	Pro	Asn	Gly	Lys	Ser	Gly	Leu	Leu	Arg	
				690				695				700				
gct	gac	tac	ttg	caa	gga	gag	aat	cct	aat	ttc	cca	agg	gtg	tta		2463
Ala	Asp	Tyr	Leu	Gln	Gly	Glu	Asn	Asn	Pro	Asn	Phe	Pro	Arg	Val	Leu	
				705				710				715				
ata	gat	gga	cca	tat	gga	gca	cca	caa	gac	tac	aag	aaa	tat	gag		2511
Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Lys	Lys	Tyr	Glu	
				720				725				730				
gtg	gtt	ttg	ttg	gta	ggt	ctt	gga	att	gga	gct	aca	cca	atg	atc	agt	2559
Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Met	Ile	Ser	
				735				740				745				
att	gtt	aaa	gac	att	gtc	aac	aac	atg	aag	gca	atg	gac	gaa	gaa	gaa	2607
Ile	Val	Lys	Asp	Ile	Val	Asn	Asn	Met	Lys	Ala	Met	Asp	Glu	Glu		
				750				755				760		765		
aat	tcc	ttg	gaa	gat	gga	cac	aat	aat	aat	atg	gca	cca	aat	tct	agc	2655
Asn	Ser	Leu	Glu	Asp	Gly	His	Asn	Asn	Asn	Met	Ala	Pro	Asn	Ser	Ser	
				770				775				780				
ccc	aat	att	gca	aaa	aat	aag	ggt	aat	aaa	tca	ggt	tca	gca	agt	gga	2703
Pro	Asn	Ile	Ala	Lys	Asn	Lys	Gly	Asn	Lys	Ser	Gly	Ser	Ala	Ser	Gly	
				785				790				795				
gga	aat	aat	ttc	aat	aca	agg	aga	gca	tat	ttc	tat	tgg	gtt	act	aga	2751
Gly	Asn	Asn	Phe	Asn	Thr	Arg	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	
				800				805				810				
gaa	caa	ggt	tca	ttt	gat	tgg	ttc	aaa	ggt	ata	atg	aat	gaa	gct	gct	2799
Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Ile	Met	Asn	Glu	Ala	Ala	

815	820	825	
gaa atg gac cat aag gga gta att gaa atg cat aat tat tgt act agt			2847
Glu Met Asp His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser			
830	835	840	845
gtt tat gaa gaa ggt gat gct cgt tct gct ctt att act atg ctt cag			2895
Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln			
850	855	860	
tct ctt cac cat gcc aaa aat ggt gtt gac att gtc tct ggc acc aga			2943
Ser Leu His His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg			
865	870	875	
gtt aag tca cat ttt gct aaa cct aat tgg cgt aat gtc tac aaa cgc			2991
Val Lys Ser His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg			
880	885	890	
att gct ctc aac cac cct gag gct aaa gtt ggg gtc ttc tat tgt ggg			3039
Ile Ala Leu Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly			
895	900	905	
gca cca gca ctg acc aaa gaa cta aga caa cac gcc ttg gat ttt tca			3087
Ala Pro Ala Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser			
910	915	920	925
cac aag aca tct acc aag ttt gat ttc cat aaa gaa aat ttt			3129
His Lys Thr Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe			
930	935		
tgagcaaaga atagaccatt aagcagagca ttaaaaatttc atcaaaaacag ctaaggacac 3189			
aggttgtttt atagaagtct accaactctc cctattgtgt acagataatg ttgcacttca 3249			
agttgatata tagttgtggt tgtgatgcta gtatattaca aaataataag attatttta 3309			
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<210> 16
<211> 939
<212> PRT
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<220>
<221> misc_feature
<222> (547)..(547)
<223> The 'Xaa' at location 547 stands for Tyr, Cys, Ser, or Phe.

<400> 16

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Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser Gly Pro Leu			
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Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn			
35	40	45	
Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr Gly Gly Lys			
50	55	60	
Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val Arg Glu Asp			
65	70	75	80
Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu			
85	90	95	
Asp Pro Glu Leu Ala Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr			
100	105	110	
Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val			
115	120	125	
Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg Pro Ile Pro			
130	135	140	
Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His Ala Leu Lys			
145	150	155	160
Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ala Ala			
165	170	175	
Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr Gly Leu Leu			

180	185	190
Pro Arg Ala Lys Phe Gly Glu Cys Ile Gly Met Asn Lys	Glu Ser Lys	
195	200	205
Glu Phe Ala Val Glu Leu Tyr Asp Ala Leu Ala Arg	Arg Arg Arg Asn Ile	
210	215	220
Thr Thr Asp Ser Ile Asn Lys Ala Gln Leu Lys	Glu Phe Trp Asp Gln	
225	230	235
Val Ala Asp Gln Ser Phe Asp Ser Arg	Leu Gln Thr Phe Phe Asp Met	
245	250	255
Val Asp Lys Asp Ala Asp Gly Arg Ile	Thr Glu Glu Glu Val Arg Glu	
260	265	270
Ile Ile Gly Leu Ser Ala Ser Ala Asn Arg Leu Ser	Thr Ile Gln Lys	
275	280	285
Gln Ala Asp Glu Tyr Ala Ala Met Ile Met	Glu Glu Leu Asp Pro Asn	
290	295	300
Asn Leu Gly Tyr Ile Met Ile Glu Asn Leu Glu	Met Leu Leu Leu Gln	
305	310	315
Ala Pro Asn Gln Ser Val Gln Arg Gly	Gly Glu Ser Arg Asn Leu Ser	
325	330	335
Gln Met Leu Ser Gln Lys Leu Lys His	Thr Gln Glu Arg Asn Pro Ile	
340	345	350
Val Arg Trp Tyr Lys Ser Phe Met Tyr Phe Leu Leu	Asp Asn Trp Gln	
355	360	365
Arg Val Trp Val Leu Leu Leu Trp Ile Gly Ile Met	Ala Gly Leu Phe	
370	375	380
Thr Trp Lys Tyr Ile Gln Tyr Lys Glu Lys Ala	Ala Tyr Lys Val Met	
385	390	395
Gly Pro Cys Val Cys Phe Ala Lys Gly Ala Ala	Glu Thr Leu Lys Leu	
405	410	415
Asn Met Ala Ile Ile Leu Phe Pro Val Cys Arg Asn	Thr Ile Thr Trp	
420	425	430
Leu Arg Asn Lys Thr Arg Leu Gly Ala Ala Val Pro	Phe Asp Asp Asn	
435	440	445
Leu Asn Phe His Lys Val Ile Ala Val Ala Ile Ala	Leu Gly Val Gly	
450	455	460
Ile His Gly Leu Ser His Leu Thr Cys Asp Phe	Pro Arg Leu Leu Asn	
465	470	475
Ala Ser Glu Glu Tyr Glu Pro Met Lys Tyr Tyr Phe	Gly Asp Gln	
485	490	495
Pro Glu Ser Tyr Trp Trp Phe Ile Lys Gly Val Glu	Gly Val Thr Gly	
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Ile Ile Met Val Val Leu Met Ala Ile Ala Phe Thr	Leu Ala Thr Pro	
515	520	525
Trp Phe Arg Arg Asn Arg Val Ser Leu Pro Lys Pro	Phe His Lys Leu	
530	535	540
Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His	Leu Phe Val Ile Val	
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Tyr Thr Leu Phe Ile Val His Gly Glu Lys Leu Tyr	Ile Thr Lys Asp	
565	570	575
Trp Tyr Lys Arg Thr Asp Met Asp Val Leu Leu Thr	Ile Pro Ile Ile	
580	585	590
Leu Tyr Ala Ser Glu Arg Leu Ile Arg Ala Phe Arg	Ser Ser Ile Lys	
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Ala Val Lys Ile Leu Lys Val Ala Val Tyr Pro	Gly Asn Val Leu Ala	
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Leu His Met Ser Lys Pro Gln Gly Tyr Lys Tyr	Lys Ser Gly Gln Tyr	
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Met Phe Val Asn Cys Ala Ala Val Ser Pro Phe	Glu Trp His Pro Phe	
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Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser	Val His Ile Arg	
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Thr	Leu	Gly	Asp	Trp	Thr	Arg	Gln	Leu	Lys	Thr	Val	Phe	Ser	Glu	Val
	675					680					685				
Cys	Gln	Pro	Pro	Pro	Asn	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Tyr
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Leu	Gln	Gly	Glu	Asn	Asn	Pro	Asn	Phe	Pro	Arg	Val	Leu	Ile	Asp	Gly
	705					710			715						720
Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Lys	Lys	Tyr	Glu	Val	Val	Leu
						725			730			735			
Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Met	Ile	Ser	Ile	Val	Lys
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Asp	Ile	Val	Asn	Asn	Met	Lys	Ala	Met	Asp	Glu	Glu	Glu	Asn	Ser	Leu
						755		760			765				
Glu	Asp	Gly	His	Asn	Asn	Asn	Met	Ala	Pro	Asn	Ser	Ser	Pro	Asn	Ile
						770		775			780				
Ala	Lys	Asn	Lys	Gly	Asn	Lys	Ser	Gly	Ser	Ala	Ser	Gly	Gly	Asn	Asn
	785					790				795					800
Phe	Asn	Thr	Arg	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly
						805			810			815			
Ser	Phe	Asp	Trp	Phe	Lys	Gly	Ile	Met	Asn	Glu	Ala	Ala	Glu	Met	Asp
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His	Lys	Gly	Val	Ile	Glu	Met	His	Asn	Tyr	Cys	Thr	Ser	Val	Tyr	Glu
						835		840			845				
Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu	Gln	Ser	Leu	His
						850		855			860				
His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr	Arg	Val	Lys	Ser
	865					870			875			880			
His	Phe	Ala	Lys	Pro	Asn	Trp	Arg	Asn	Val	Tyr	Lys	Arg	Ile	Ala	Leu
						885			890			895			
Asn	His	Pro	Glu	Ala	Lys	Val	Gly	Val	Phe	Tyr	Cys	Gly	Ala	Pro	Ala
						900		905			910				
Leu	Thr	Lys	Glu	Leu	Arg	Gln	His	Ala	Leu	Asp	Phe	Ser	His	Lys	Thr
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<212> DNA
<213> Oryza sativa
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<221> CDS
<222> (1)..(2529)
<223> coding for NADPH oxidase

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Gly Leu Pro Arg Pro Pro Gly Ala Gly Ala Gly Ala Ala Gly Gly
20 25 30
ttc gcg cgg ggg ctg atg aag cag ccg tcg ccg ctg gcg tcc ggg gtg 144
Phe Ala Arg Gly Leu Met Lys Gln Pro Ser Arg Leu Ala Ser Gly Val
35 40 45
agg cag ttc gcg tcg agg gtg tcg atg aag gtg ccg gag ggg gtg ggg 192
Arg Gln Phe Ala Ser Arg Val Ser Met Lys Val Pro Glu Gly Val Gly
50 55 60
ggg atg cgg ccc ggt ggc ggg agg atg acg ccg atg cag tcc agc gcg 240
Gly Met Arg Pro Gly Gly Arg Met Thr Arg Met Gln Ser Ser Ala
65 70 75 80

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cag	gtg	ggg	ctc	cg	gg	ctc	cg	tc	gac	aag	ac	tc	gg	gc	gg	288	
Gln	Val	Gly	Leu	Arg	Gly	Leu	Arg	Phe	Leu	Asp	Lys	Thr	Ser	Gly	Gly		
85						90									95		
aag	gag	ggg	tgg	aag	tcc	gtc	gag	cg	cg	tc	gac	gag	at	ac	cg	336	
Lys	Glu	Gly	Trp	Lys	Ser	Val	Glu	Arg	Arg	Phe	Asp	Glu	Met	Asn	Arg		
100						105									110		
aac	gg	cg	ctc	cc	aag	gag	ag	tc	gg	aag	tg	atc	gg	at	gg	384	
Asn	Gly	Arg	Leu	Pro	Lys	Glu	Ser	Phe	Gly	Lys	Cys	Ile	Gly	Met	Gly		
115						120									125		
gac	tcc	aag	gag	ttc	gg	gg	gag	ct	tg	g	cg	ct	gg	cg	gg	432	
Asp	Ser	Lys	Glu	Phe	Ala	Gly	Glu	Leu	Phe	Val	Ala	Leu	Ala	Arg	Arg		
130						135									140		
agg	aa	ct	gag	cc	gg	gag	gac	gg	atc	ac	aag	gag	cag	ct	aag	480	
Arg	Asn	Leu	Glu	Pro	Glu	Asp	Gly	Ile	Thr	Lys	Glu	Gln	Leu	Lys	Glu		
145						150									160		
ttc	tgg	gag	gag	at	g	ac	g	ac	tcc	gac	tc	cg	cg	ct	cg	528	
Phe	Trp	Glu	Glu	Met	Thr	Asp	Gln	Asn	Phe	Asp	Ser	Arg	Leu	Arg	Ile		
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ttc	ttt	gac	at	g	tc	gac	aag	aa	gg	at	g	ct	ac	gaa	gat	576	
Phe	Phe	Asp	Met	Cys	Asp	Lys	Asn	Gly	Asp	Gly	Met	Leu	Thr	Glu	Asp		
180						185									190		
gag	gtc	aag	gag	gtt	att	ata	ct	tg	at	g	cg	aa	ct	g	cg	624	
Glu	Val	Lys	Glu	Val	Ile	Ile	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ala		
195						200									205		
aag	ct	g	aag	gg	ca	g	cg	ac	tg	ac	tg	at	tg	gag	gag	672	
Lys	Leu	Lys	Gly	His	Ala	Ala	Thr	Tyr	Ala	Ser	Leu	Ile	Met	Glu	Glu		
210						215									220		
ct	g	ac	cc	g	ac	cg	gg	tg	atc	g	atc	tg	cg	ct	gag	720	
Leu	Asp	Pro	Asp	Asp	Arg	Gly	Tyr	Ile	Glu	Ile	Trp	Gln	Leu	Glu	Thr		
225						230									240		
ct	ct	cg	gg	at	g	tg	ag	g	cg	tg	cg	gag	aag	at	gag	768	
Leu	Leu	Arg	Gly	Met	Val	Ser	Ala	Gln	Ala	Ala	Pro	Glu	Lys	Met	Lys		
245						250									255		
cg	ac	ac	tc	g	cg	gg	ac	at	tg	atc	cc	tg	cg	tg	cg	816	
Arg	Thr	Thr	Ser	Ser	Leu	Ala	Arg	Thr	Met	Ile	Pro	Ser	Arg	Tyr	Arg		
260						265									270		
agc	cc	ct	aag	cg	ca	gt	tc	gg	ac	tg	tc	gt	ca	g	g	864	
Ser	Pro	Leu	Lys	Arg	His	Val	Ser	Arg	Thr	Val	Asp	Phe	Val	His	Glu		
275						280									285		
aa	tgg	aag	cg	atc	tgg	ctc	gtc	g	ct	tg	cc	tg	cg	tg	cg	912	
Asn	Trp	Lys	Arg	Ile	Trp	Leu	Val	Ala	Leu	Trp	Leu	Ala	Val	Asn	Val		
290						295									300		
gg	ct	tcc	gg	tac	aag	ttc	gag	c	ag	tg	ac	tg	cc	gg	ttc	960	
Gly	Leu	Phe	Ala	Tyr	Lys	Phe	Glu	Gln	Tyr	Glu	Arg	Arg	Ala	Ala	Phe		
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Gln	Val	Met	Gly	His	Cys	Val	Cys	Val	Ala	Lys	Gly	Ala	Ala	Glu	Val		
325						330									335		
ctc	aag	ctc	aa	at	g	cg	ctc	atc	ctc	ccc	gt	tg	cg	aa	ac	1056	
Leu	Lys	Leu	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr		
340						345									350		
ctc	acc	ac	ctc	agg	tcc	ac	cg	ctc	ag	ca	gt	atc	cc	ttc	gac	1104	
Leu	Thr	Thr	Leu	Arg	Ser	Thr	Ala	Leu	Ser	His	Val	Ile	Pro	Phe	Asp		
355						360									365		
gac	aa	atc	aa	tcc	ca	aag	gt	atc	cg	cg	ac	atc	gg	cc	gg	1152	
Asp	Asn	Ile	Asn	Phe	His	Lys	Val	Ile	Ala	Ala	Thr	Ile	Ala	Ala	Ala		
370						375									380		
acc	gg	gt	ca	ac	ct	cg	ca	gt	ac	tg	gac	ttc	cc	ag	ct	1200	
Thr	Ala	Val	His	Thr	Leu	Ala	His	Val	Thr	Cys	Asp	Phe	Pro	Arg	Leu		
385						390									400		
atc	aa	tgc	cc	ac	gac	aag	ttc	at	g	cg	ac	tg	gg	cc	aa	ttc	1248

Ile Asn Cys Pro Ser Asp Lys Phe Met Ala Thr Leu Gly Pro Asn Phe	405	410	415	
Gly Tyr Arg Gln Pro Thr Tyr Ala Asp Leu Leu Glu Ser Ala Pro Gly	420	425	430	1296
gtc acc ggc atc ctc atg atc atc atg tcc ttc tcc ttc acg ctg				1344
Val Thr Gly Ile Leu Met Ile Ile Met Ser Phe Ser Phe Thr Leu	435	440	445	
gcc acg cac tcc ttc cgc cg ^g agc gtc aag ctg ccg tcg ccg ctg				1392
Ala Thr His Ser Phe Arg Arg Ser Val Val Lys Leu Pro Ser Pro Leu	450	455	460	
cac cac ctc gcc ggc ttc aac gcc ttc tgg tac g ^c g ^c cac cac ctc ctg				1440
His His Leu Ala Gly Phe Asn Ala Phe Trp Tyr Ala His His Leu Leu	465	470	475	
gtg ctc gcc tac gtc ctc gtc gtg cac tcc tac ttc ata ttc ctc				1488
Val Leu Ala Tyr Val Leu Leu Val Val His Ser Tyr Phe Ile Phe Leu	485	490	495	
acc agg gag tgg tac aag aaa acg aca tgg atg tac ctg ata gtc cca				1536
Thr Arg Glu Trp Tyr Lys Lys Thr Thr Trp Met Tyr Leu Ile Val Pro	500	505	510	
gtg ctc ttc tat gca tgc gag aga acg atc aga aaa gtt cga gag aac				1584
Val Leu Phe Tyr Ala Cys Glu Arg Thr Ile Arg Lys Val Arg Glu Asn	515	520	525	
aac tac cgc gtg agc atc gtc aag gca g ^c att tac cca gga aat gtg				1632
Asn Tyr Arg Val Ser Ile Val Lys Ala Ala Ile Tyr Pro Gly Asn Val	530	535	540	
ctc tct ctt cac atg aag aag ccg ccg ggt ttc aag tac aag agc ggg				1680
Leu Ser Leu His Met Lys Lys Pro Pro Gly Phe Lys Tyr Lys Ser Gly	545	550	555	
atg tac ctg ttt gtg aag tgc cct gat gtc tct cct ttc gaa tgg cat				1728
Met Tyr Leu Phe Val Lys Cys Pro Asp Val Ser Pro Phe Glu Trp His	565	570	575	
ccc ttc tcc atc act tct gca cct gga gat gac tac ctg agt gtg cat				1776
Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His	580	585	590	
atc cgt aca cta ggt gac tgg acg act gaa ctc aga aac ctg ttt ggg				1824
Ile Arg Thr Leu Gly Asp Trp Thr Thr Glu Leu Arg Asn Leu Phe Gly	595	600	605	
aag gct tgc gag gca cag gtt act tct aag aag gct acc ctt tca aga				1872
Lys Ala Cys Glu Ala Gln Val Thr Ser Lys Lys Ala Thr Leu Ser Arg	610	615	620	
ctt gaa act aca gtt gtg g ^c gac gct cag aca gag gat act agg ttt				1920
Leu Glu Thr Thr Val Val Ala Asp Ala Gln Thr Glu Asp Thr Arg Phe	625	630	635	
cct aag gtc ctt att gat ggg ccc tat ggt gca ccg g ^c caa aac tac				1968
Pro Lys Val Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asn Tyr	645	650	655	
aag aag tat gac att ctt ttg ctt att ggt ctt gga att ggt gct act				2016
Lys Lys Tyr Asp Ile Leu Leu Ile Gly Leu Gly Ile Gly Ala Thr	660	665	670	
cct ttc atc agc att ctg aag gat ctg ttg aac aac att aaa tcc aac				2064
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Lys Ser Asn	675	680	685	
gaa gag gtg gaa agc ata cat ggt tct gag ata ggc agc ttc aag aac				2112
Glu Glu Val Glu Ser Ile His Gly Ser Glu Ile Gly Ser Phe Lys Asn	690	695	700	
aat ggg cca gga aga gct tac ttc tac tgg gtg acc aga gag caa ggg				2160
Asn Gly Pro Gly Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly	705	710	715	
tcc ttc gag tgg ttt aaa gga gtc atg aac gat gtc gct gaa agt gat				2208
Ser Phe Glu Trp Phe Lys Gly Val Met Asn Asp Val Ala Glu Ser Asp				

725	730	735	
cac aat aat att ata gag atg cac aat	730 tac ctg acc agc gtg tat gaa	735	2256
His Asn Asn Ile Ile Glu Met His Asn	Tyr Leu Thr Ser Val Tyr Glu		
740	745	750	
gaa ggc gac gca agg tca gct ttg att	gcc atg gtt cag tca ctt caa		2304
Glu Gly Asp Ala Arg Ser Ala Leu Ile	Ala Met Val Gln Ser Leu Gln		
755	760	765	
cat gcc aaa aat ggt gtg gat atc gtc	tcc ggc agc agg att cgc aca		2352
His Ala Lys Asn Gly Val Asp Ile Val	Ser Gly Ser Arg Ile Arg Thr		
770	775	780	
cat ttt gcg agg cct aac tgg aga aag	gtg ttc tct gac ttg gcg aat		2400
His Phe Ala Arg Pro Asn Trp Arg Lys	Val Phe Ser Asp Leu Ala Asn		
785	790	795	800
gcc cac aaa aac tca cgc ata ggt gtt	ttc tat tgt gga tcc cct aca		2448
Ala His Lys Asn Ser Arg Ile Gly Val	Phe Tyr Cys Gly Ser Pro Thr		
805	810	815	
ctc acg aaa caa ctc aag gat ctt tca	aaa gaa ttc agc cag aca acc		2496
Leu Thr Lys Gln Leu Lys Asp Leu Ser	Lys Glu Phe Ser Gln Thr Thr		
820	825	830	
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Thr Thr Arg Phe His Phe His Lys Glu	Asn Phe		
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<211> 843

<212> PRT

<213> Oryza sativa

<400> 18

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Arg Gln Phe Ala Ser Arg Val Ser Met Lys Val Pro Glu Gly Val Gly			
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Gly Met Arg Pro Gly Gly Arg Met Thr Arg Met Gln Ser Ser Ala			
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Gln Val Gly Leu Arg Gly Leu Arg Phe Leu Asp Lys Thr Ser Gly Gly			
85	90	95	
Lys Glu Gly Trp Lys Ser Val Glu Arg Arg Phe Asp Glu Met Asn Arg			
100	105	110	
Asn Gly Arg Leu Pro Lys Glu Ser Phe Gly Lys Cys Ile Gly Met Gly			
115	120	125	
Asp Ser Lys Glu Phe Ala Gly Glu Leu Phe Val Ala Leu Ala Arg Arg			
130	135	140	
Arg Asn Leu Glu Pro Glu Asp Gly Ile Thr Lys Glu Gln Leu Lys Glu			
145	150	155	160
Phe Trp Glu Glu Met Thr Asp Gln Asn Phe Asp Ser Arg Leu Arg Ile			
165	170	175	
Phe Phe Asp Met Cys Asp Lys Asn Gly Asp Gly Met Leu Thr Glu Asp			
180	185	190	
Glu Val Lys Glu Val Ile Ile Leu Ser Ala Ser Ala Asn Lys Leu Ala			
195	200	205	
Lys Leu Lys Gly His Ala Ala Thr Tyr Ala Ser Leu Ile Met Glu Glu			
210	215	220	
Leu Asp Pro Asp Asp Arg Gly Tyr Ile Glu Ile Trp Gln Leu Glu Thr			
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Leu Leu Arg Gly Met Val Ser Ala Gln Ala Ala Pro Glu Lys Met Lys			
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Arg Thr Thr Ser Ser Leu Ala Arg Thr Met Ile Pro Ser Arg Tyr Arg
 260 265 270
 Ser Pro Leu Lys Arg His Val Ser Arg Thr Val Asp Phe Val His Glu
 275 280 285
 Asn Trp Lys Arg Ile Trp Leu Val Ala Leu Trp Leu Ala Val Asn Val
 290 295 300
 Gly Leu Phe Ala Tyr Lys Phe Glu Gln Tyr Glu Arg Arg Ala Ala Phe
 305 310 315 320
 Gln Val Met Gly His Cys Val Cys Val Ala Lys Gly Ala Ala Glu Val
 325 330 335
 Leu Lys Leu Asn Met Ala Leu Ile Leu Pro Val Cys Arg Asn Thr
 340 345 350
 Leu Thr Thr Leu Arg Ser Thr Ala Leu Ser His Val Ile Pro Phe Asp
 355 360 365
 Asp Asn Ile Asn Phe His Lys Val Ile Ala Ala Thr Ile Ala Ala Ala
 370 375 380
 Thr Ala Val His Thr Leu Ala His Val Thr Cys Asp Phe Pro Arg Leu
 385 390 395 400
 Ile Asn Cys Pro Ser Asp Lys Phe Met Ala Thr Leu Gly Pro Asn Phe
 405 410 415
 Gly Tyr Arg Gln Pro Thr Tyr Ala Asp Leu Leu Glu Ser Ala Pro Gly
 420 425 430
 Val Thr Gly Ile Leu Met Ile Ile Met Ser Phe Ser Phe Thr Leu
 435 440 445
 Ala Thr His Ser Phe Arg Arg Ser Val Val Lys Leu Pro Ser Pro Leu
 450 455 460
 His His Leu Ala Gly Phe Asn Ala Phe Trp Tyr Ala His His Leu Leu
 465 470 475 480
 Val Leu Ala Tyr Val Leu Leu Val Val His Ser Tyr Phe Ile Phe Leu
 485 490 495
 Thr Arg Glu Trp Tyr Lys Lys Thr Thr Trp Met Tyr Leu Ile Val Pro
 500 505 510
 Val Leu Phe Tyr Ala Cys Glu Arg Thr Ile Arg Lys Val Arg Glu Asn
 515 520 525
 Asn Tyr Arg Val Ser Ile Val Lys Ala Ala Ile Tyr Pro Gly Asn Val
 530 535 540
 Leu Ser Leu His Met Lys Lys Pro Pro Gly Phe Lys Tyr Lys Ser Gly
 545 550 555 560
 Met Tyr Leu Phe Val Lys Cys Pro Asp Val Ser Pro Phe Glu Trp His
 565 570 575
 Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His
 580 585 590
 Ile Arg Thr Leu Gly Asp Trp Thr Thr Glu Leu Arg Asn Leu Phe Gly
 595 600 605
 Lys Ala Cys Glu Ala Gln Val Thr Ser Lys Lys Ala Thr Leu Ser Arg
 610 615 620
 Leu Glu Thr Thr Val Val Ala Asp Ala Gln Thr Glu Asp Thr Arg Phe
 625 630 635 640
 Pro Lys Val Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asn Tyr
 645 650 655
 Lys Lys Tyr Asp Ile Leu Leu Ile Gly Leu Gly Ile Gly Ala Thr
 660 665 670
 Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Lys Ser Asn
 675 680 685
 Glu Glu Val Glu Ser Ile His Gly Ser Glu Ile Gly Ser Phe Lys Asn
 690 695 700
 Asn Gly Pro Gly Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly
 705 710 715 720
 Ser Phe Glu Trp Phe Lys Gly Val Met Asn Asp Val Ala Glu Ser Asp
 725 730 735
 His Asn Asn Ile Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu

740	745	750													
Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Ala	Met	Val	Gln	Ser	Leu	Gln
755							760					765			
His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Ser	Arg	Ile	Arg	Thr
770							775					780			
His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Phe	Ser	Asp	Leu	Ala	Asn
785							790				795			800	
Ala	His	Lys	Asn	Ser	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ser	Pro	Thr
							805				810			815	
Leu	Thr	Lys	Gln	Leu	Lys	Asp	Leu	Ser	Lys	Glu	Phe	Ser	Gln	Thr	Thr
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Thr	Thr	Arg	Phe	His	Phe	His	Lys	Glu	Asn	Phe					
							835				840				

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<213> *Arabidopsis thaliana*

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<223> coding for NADPH oxidase

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gaa	gcc	gga	aac	agc	gga	cca	atg	agc	ggt	ggt	caa	tta	cca	ccg	atc	96
Glu	Ala	Gly	Asn	Ser	Gly	Pro	Met	Ser	Gly	Gly	Gln	Leu	Pro	Pro	Ile	
								20				25		30		
tat	aaa	aaa	ccg	ggg	aac	tcc	aga	ttc	act	gct	gag	aac	agt	cag	aga	144
Tyr	Lys	Lys	Pro	Gly	Asn	Ser	Arg	Phe	Thr	Ala	Glu	Asn	Ser	Gln	Arg	
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aca	cgt	acg	gca	cca	tac	gtg	gac	ctc	acg	gta	gat	gta	caa	gac	gat	192
Thr	Arg	Thr	Ala	Pro	Tyr	Val	Asp	Leu	Thr	Val	Asp	Val	Gln	Asp	Asp	
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aca	gtc	tct	gta	cat	agc	ttg	aaa	atg	gaa	ggt	gga	tct	agc	gtt	gaa	240
Thr	Val	Ser	Val	His	Ser	Leu	Lys	Met	Glu	Gly	Gly	Ser	Ser	Val	Glu	
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gag	agt	ccg	gag	ctt	act	ttg	ctg	aaa	cga	aac	cgt	ctt	gag	aag	aaa	288
Glu	Ser	Pro	Glu	Leu	Thr	Leu	Leu	Lys	Arg	Asn	Arg	Leu	Glu	Lys	Lys	
								85				90		95		
aca	acg	gtg	gtg	aaa	cgt	ttg	gcg	tct	gtt	tct	cac	gag	ctt	aag	cgt	336
Thr	Thr	Val	Val	Lys	Arg	Leu	Ala	Ser	Val	Ser	His	Glu	Leu	Lys	Arg	
								100				105		110		
ttg	aca	tct	gtt	tct	ggt	ggt	att	ggt	gga	aga	aag	ccg	cct	cga	ccg	384
Leu	Thr	Ser	Val	Ser	Gly	Gly	Ile	Gly	Gly	Arg	Lys	Pro	Pro	Arg	Pro	
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aga tac aag agt gga caa tac atg tat ctc aac tgt tct gca gtt tct		1872
Arg Tyr Lys Ser Gly Gln Tyr Met Tyr Leu Asn Cys Ser Ala Val Ser		
610 615 620		
aca tta gaa tgg cat cca ttc tca att acc tca gct cca gga gat gac		1920
Thr Leu Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp		
625 630 635 640		
tac ctc agt gtc cac atc agg gtt tta gga gac tgg act aag caa tta		1968
Tyr Leu Ser Val His Ile Arg Val Leu Gly Asp Trp Thr Lys Gln Leu		
645 650 655		
aga tca tta ttc tct gag gtg tgc aag cca cgc cct cct gat gaa cac		2016
Arg Ser Leu Phe Ser Glu Val Cys Lys Pro Arg Pro Pro Asp Glu His		
660 665 670		
aga ctg aac aga gcc gac tcg aag cac tgg gat tac atc cct gac ttt		2064
Arg Leu Asn Arg Ala Asp Ser Lys His Trp Asp Tyr Ile Pro Asp Phe		
675 680 685		
cca aga atc cta att gat ggt cca tat gga gca cca gca caa gac tac		2112
Pro Arg Ile Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr		
690 695 700		
aag aag ttt gaa gtt gtt ctg cta gtg ggt cta gga atc ggt gcc act		2160
Lys Lys Phe Glu Val Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr		
705 710 715 720		
ccg atg atc agc ata gtg agt gac ata atc aat aac ttg aaa ggc gtg		2208
Pro Met Ile Ser Ile Val Ser Asp Ile Ile Asn Asn Leu Lys Gly Val		
725 730 735		
gaa gaa ggc agt aac cga aga cag tca ccg atc cat aat atg gtc aca		2256
Glu Glu Gly Ser Asn Arg Arg Gln Ser Pro Ile His Asn Met Val Thr		
740 745 750		
cct cct gtt tct cca tca aga aaa agt gag acg ttc aga acc aag aga		2304
Pro Pro Val Ser Pro Ser Arg Lys Ser Glu Thr Phe Arg Thr Lys Arg		
755 760 765		
gct tac ttc tac tgg gtc aca aga gag cag ggg tcg ttt gac tgg ttc		2352
Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe		
770 775 780		
aag aac gtg atg gac gaa gtg act gaa aca gac cgc aaa aac gta att		2400
Lys Asn Val Met Asp Glu Val Thr Glu Thr Asp Arg Lys Asn Val Ile		
785 790 795 800		
gag ctg cat aat tac tgc acc agc gtt tac gag gaa ggg gac gcg agg		2448
Glu Leu His Asn Tyr Cys Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg		
805 810 815		
tct gca ctt atc acg atg ctc cag tct cta aac cat gct aag cat gga		2496
Ser Ala Leu Ile Thr Met Leu Gln Ser Leu Asn His Ala Lys His Gly		
820 825 830		
gtg gac gtt gtg tca gga aca cgt gtc atg tcc cat ttc gct agg cca		2544
Val Asp Val Val Ser Gly Thr Arg Val Met Ser His Phe Ala Arg Pro		
835 840 845		
aac tgg aga agc gtt ttc aaa agg atc gct gtg aat cat cct aag act		2592
Asn Trp Arg Ser Val Phe Lys Arg Ile Ala Val Asn His Pro Lys Thr		
850 855 860		
aga gtc gga gtg ttt tat tgt gga gca gct ggg tta gtg aaa gag tta		2640
Arg Val Gly Val Phe Tyr Cys Gly Ala Ala Gly Leu Val Lys Glu Leu		
865 870 875 880		
cga cac tta tca ctg gat ttc tct cat aag acc tcc acc aag ttc atc		2688
Arg His Leu Ser Leu Asp Phe Ser His Lys Thr Ser Thr Lys Phe Ile		
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Phe His Lys Glu Asn Phe
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Ala Thr Thr Ser Asn Tyr Tyr Gly Glu Asp Glu Pro Tyr Val Glu Ile
35 40 45
Thr Leu Asp Ile His Asp Asp Ser Val Ser Val Tyr Gly Leu Lys Ser
50 55 60
Pro Asn His Arg Gly Ala Gly Ser Asn Tyr Glu Asp Gln Ser Leu Leu
65 70 75 80
Arg Gln Gly Arg Ser Gly Arg Ser Asn Ser Val Leu Lys Arg Leu Ala
85 90 95
Ser Ser Val Ser Thr Gly Ile Thr Arg Val Ala Ser Ser Val Ser Ser
100 105 110
Ser Ser Ala Arg Lys Pro Pro Arg Pro Gln Leu Ala Lys Leu Arg Arg
115 120 125
Ser Lys Ser Arg Ala Glu Leu Ala Leu Lys Gly Leu Lys Phe Ile Thr
130 135 140
Lys Thr Asp Gly Val Thr Gly Trp Pro Glu Val Glu Lys Arg Phe Tyr
145 150 155 160
Val Met Thr Met Thr Asn Asn Gly Leu Leu His Arg Ser Arg Phe Gly
165 170 175
Glu Cys Ile Gly Met Lys Ser Thr Glu Phe Ala Leu Ala Leu Phe Asp
180 185 190
Ala Leu Ala Arg Arg Glu Asn Val Ser Gly Asp Ser Ile Asn Met Asn
195 200 205
Glu Leu Lys Glu Phe Trp Lys Gln Ile Thr Asp Gln Asp Phe Asp Ser
210 215 220
Arg Leu Arg Thr Phe Phe Ala Met Val Asp Lys Asp Ser Asp Gly Arg
225 230 235 240
Leu Asn Glu Ala Glu Val Arg Glu Ile Ile Thr Leu Ser Ala Ser Ala
245 250 255
Asn Glu Leu Asp Asn Ile Arg Arg Gln Ala Asp Glu Tyr Ala Ala Leu
260 265 270
Ile Met Glu Glu Leu Asp Pro Tyr His Tyr Gly Tyr Ile Met Ile Glu
275 280 285
Asn Leu Glu Ile Leu Leu Leu Gln Ala Pro Met Gln Asp Val Arg Asp
290 295 300
Gly Glu Ser Lys Lys Leu Ser Lys Met Leu Ser Gln Asn Leu Met Val
305 310 315 320
Pro Gln Ser Arg Asn Leu Gly Ala Arg Phe Cys Arg Gly Met Lys Tyr
325 330 335
Phe Leu Phe Asp Asn Trp Lys Arg Val Trp Val Met Ala Leu Trp Ile
340 345 350
Gly Ala Met Ala Gly Leu Phe Thr Trp Lys Phe Met Glu Tyr Arg Lys
355 360 365
Arg Ser Ala Tyr Glu Val Met Gly Val Cys Val Cys Ile Ala Lys Gly
370 375 380
Ala Ala Glu Thr Leu Lys Leu Asn Met Ala Met Ile Leu Leu Pro Val
385 390 395 400
Cys Arg Asn Thr Ile Thr Trp Leu Arg Thr Lys Thr Lys Leu Ser Ala
405 410 415

Ile Val Pro Phe Asp Asp Ser Leu Asn Phe His Lys Val Ile Ala Ile
 420 425 430
 Gly Ile Ser Val Gly Val Gly Ile His Ala Thr Ser His Leu Ala Cys
 435 440 445
 Asp Phe Pro Arg Leu Ile Ala Ala Asp Glu Asp Gln Tyr Glu Pro Met
 450 455 460
 Glu Lys Tyr Phe Gly Pro Gln Thr Lys Arg Tyr Leu Asp Phe Val Gln
 465 470 475 480
 Ser Val Glu Gly Val Thr Gly Ile Gly Met Val Val Leu Met Thr Ile
 485 490 495
 Ala Phe Thr Leu Ala Thr Thr Trp Phe Arg Arg Asn Lys Leu Asn Leu
 500 505 510
 Pro Gly Pro Leu Lys Lys Ile Thr Gly Phe Asn Ala Phe Trp Tyr Ser
 515 520 525
 His His Leu Phe Val Ile Val Tyr Ser Leu Leu Val Val His Gly Phe
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 Tyr Val Tyr Leu Ile Ile Glu Pro Trp Tyr Lys Lys Thr Thr Trp Met
 545 550 555 560
 Tyr Leu Met Val Pro Val Val Leu Tyr Leu Cys Glu Arg Leu Ile Arg
 565 570 575
 Ala Phe Arg Ser Ser Val Glu Ala Val Ser Val Leu Lys Val Ala Val
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 595 600 605
 Arg Tyr Lys Ser Gly Gln Tyr Met Tyr Leu Asn Cys Ser Ala Val Ser
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 Thr Leu Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp
 625 630 635 640
 Tyr Leu Ser Val His Ile Arg Val Leu Gly Asp Trp Thr Lys Gln Leu
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 Arg Leu Asn Arg Ala Asp Ser Lys His Trp Asp Tyr Ile Pro Asp Phe
 675 680 685
 Pro Arg Ile Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr
 690 695 700
 Lys Lys Phe Glu Val Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr
 705 710 715 720
 Pro Met Ile Ser Ile Val Ser Asp Ile Ile Asn Asn Leu Lys Gly Val
 725 730 735
 Glu Glu Gly Ser Asn Arg Arg Gln Ser Pro Ile His Asn Met Val Thr
 740 745 750
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 Lys Asn Val Met Asp Glu Val Thr Glu Thr Asp Arg Lys Asn Val Ile
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